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Plants with reduced activity of a Class 3 branching enzyme

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Description

- The present invention relates to plant cells and plants, which are genetically modified, wherein the genetic modification leads to the reduction of the activity of a Class 3 vegetable branching enzyme in comparison with corresponding wild type plant cells or wild type plants that have not been genetically modified. Furthermore, the present invention relates to means and methods for the manufacture of such plant cells and plants. Plant cells and plants of this type synthesise a modified starch. The present invention therefore also relates to the starch synthesised by the plant cells and plants according to the invention as well as to methods for the manufacture of the starch and to the manufacture of starch derivatives of this starch. Furthermore, the present invention relates to nucleic acids coding a Class 3 branching enzyme, vectors, host cells, plant cells and plants containing such nucleic acid molecules.
- With regard to the increasing importance currently attributed to vegetable constituents as renewable raw material sources, one of the tasks of biotechnological research is to endeavour to adapt these vegetable raw materials to suit the requirements of the processing industry. Furthermore, in order to enable regenerating raw materials to be used in as many areas of application as possible, it is necessary to achieve a large variety of materials.

- Polysaccharide starch is made up of chemically uniform base components, the glucose molecules, but constitutes a complex mixture of different molecule forms, which exhibit differences with regard to the degree of polymerisation and branching, and therefore differ strongly from one another in their physical-chemical characteristics. Discrimination is made between amylose starch, an essentially unbranched polymer made from α -1,4-glycosidically linked glucose units, and the

amylopectin starch", a branched polymer, in which the branches come about by the occurrence of additional α -1,6-glycosidic links. A further essential difference between amylose and amylopectin lies in the molecular weight. While amylose, depending on the origin of the starch, has a molecular weight of $5 \times 10^5 - 10^6$ Da, that of the amylopectin lies between 10^7 and 10^8 Da. The two macromolecules can be differentiated by their molecular weight and their different physical-chemical characteristics, which can most easily be made visible by their different iodine bonding characteristics.

10 Amylose has long been looked upon as a linear polymer, consisting of α -1,4-glycosidically linked α -D-glucose monomers. In more recent studies, however, the presence of α -1,6-glycosidic branching points (ca. 0.1%) has been shown (Hizukuri and Takagi, Carbohydr. Res. 134, (1984), 1-10; Takeda et al., Carbohydr. Res. 132, (1984), 83-92).

15 Amylopectin constitutes a complex mixture of differently branched glucose chains. In contrast to amylose, amylopectin is more strongly branched. According to textbook information (Voet and Voet, Biochemistry, John Wiley & Sons, 1990), on average, the α -1,6 branches occur every 24 to 30 glucose residues. This is equivalent to a degree of branching of ca. 3% - 4%. The figures for the degree of branching are variable and are dependent on the origin (e.g. plant species, plant type etc.) of the appropriate starch. In typical plants used for the industrial production of starch, such as maize, wheat or potato, for example, the synthesised starch consists of ca. 20% - 30% amylose starch and ca. 70% - 80% amylopectin starch.

25 The functional characteristics of the starch, along with the amylose/amylopectin ratio and the phosphate content, are strongly affected by the molecular weight, the pattern of the side chain distribution, the ion concentration, the lipid and protein content, the average grain size of the starch and the grain morphology of the starch etc. At the same time, by way of example, the solubility, the retrogradation behaviour, the water bonding capability, the film formation characteristics, the viscosity, the sticking characteristics, the freezing-thawing stability, the acid stability, the gelling strength

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etc. must be mentioned as important functional characteristics. The grain size of the starch can also be important for different applications.

Branching enzymes, which are also abbreviated by the designation "BE" (from
5 Branching Enzyme; E.C. 2.4.1.18), catalyse the introduction of α -1,6 branches in α -
1,4-glucans. Branching enzymes and the nucleic or amino acid sequences that
characterise them are known from widely different organisms, such as bacteria,
microbial fungi, mammals, algae and higher plants, for example. As only plants
synthesise starch, while the above-mentioned non-vegetable organisms (e.g.
10 bacteria, fungi and mammals) synthesise glycogen, the related branching enzymes,
which are involved in the synthesis of the appropriate polymer, can also be sub-
divided into glycogen branching enzymes and starch branching enzymes. Plants are
therefore starch branching enzymes, which are often also referred to as Q-enzymes
in older literature.

15 In all plant species that have been investigated up to now, the branching enzymes described can be associated with two different classes (Burton et al., 1995, Plant Journal 7, 3-15; Mizuno et al., 2001, Plant Cell Physiol. 42(4), 349-357). The association with these classes, sometimes designated in the literature with A or 2
20 respectively and B or 1 respectively, is based on the comparison of derived protein sequences.

As different nomenclatures have been used in the past for designating and classifying branching enzymes, Smith-White and Preiss (1994, Plant Molecular Biology Reporter 12, 67-71) (1994, Plant Molecular Biology Reporter 12, 67-71) have proposed a system for standardising this nomenclature, in which the association with the two classes of vegetable branching enzymes is also based on the comparison of derived protein sequences (Larsson et al., 1998, Plant Mol. Biol. 37, 505-511). According to this nomenclature, those vegetable branching enzymes, the amino acid sequence of which has a higher degree of identity with that of branching enzyme I of maize (GenBank Acc: D11081), is to be designated as a Class 1 branching enzyme, and those vegetable branching enzymes, the coding amino acid sequence of which has a higher degree of identity with that of branching enzyme II of maize (GenBank

Acc: AF072725), is to be designated as a Class 2 branching enzyme. The designation of gene products, which are coding for branching enzymes, are, in accordance with the nomenclature of Smith-White and Preiss, to be incorporated in the already existing nomenclature by means of E.C. numbers. This results in the so-called GPN (Gene Product Number) Codes for the two classes, namely GPN 2.2.4.1.18:1 for Class 1 branching enzymes and GPN 2.2.4.18:2 for Class 2 branching enzymes.

The following vegetable or starch branching enzymes therefore belong to Class 1 (GPN 2.2.1.18:1) according to the nomenclature proposed by Smith-White and Preiss (1994, Plant Molecular Biology Reporter 12, 67-71):

BE I from *Aegilops tauschii* (GenBank Acc: AF525746), BE I from barley (GenBank Acc: AY304541), BE from tapioca (GenBank Acc: X77012), BE I (frequently also described as BE 1) from rice (GenBank Acc: D11082, D10752, D10838), BE 3 from bean (GenBank Acc: AB029549), BE II from pea (GenBank Acc: X80010), BE from millet (GenBank Acc: AF169833), BE I from potato (GenBank Acc: Y08786, X69805), BE from wheat (GenBank Acc: Y12320, AF076679, AF002820) and BE I from maize (GenBank Acc: D11081, AAO20100, E03435, AY176762, U17897, AF072724).

At the same time, the amino acid sequences for different Class 1 branching enzymes each have an identity of more than 60% with the amino acid sequence of branching enzyme I from maize (GenBank Acc: D11081).

Branching enzymes, which belong to Class 2 (GPN 2.2.1.18:2) according to the nomenclature proposed by Smith-White and Preiss (1994, Plant Molecular Biology Reporter 12, 67-71) are, for example, BE IIa from *Aegilops tauschii* (GenBank Acc: AF338431, WO 9914314), BE2-1 and BE2-2 from *Arabidopsis thaliana* (BE2-1 GenBank Acc: NM_129196 CAA04134; BE2-2 GenBank Acc: CAB82930, NM_120446), BE IIa and BE IIb from barley (BE IIa GenBank Acc: AF064560; BE IIb GenBank Acc: AF064561), BE II from sweet potato (GenBank Acc: AB071286), BE III and BE IV (frequently also described as BE 3 or BE 4 respectively) from rice (BE III GenBank Acc: D16201; BE IV GenBank Acc: AB023498), BE 1 from bean (GenBank Acc: AB029548), BE I from pea (GenBank Acc: X80009), BE IIb from millet (GenBank Acc: AY304540), BE II from potato (GenBank Acc: AJ000004,

AJ011885, AJ011888, AJ011889, AJ011890), BE II or BE IIa from wheat (GenBank Acc: Y11282, AF286319, AF338432, U66376) and BE II, or BE IIb from maize (BE II GenBank Acc: AAA18571, T02981; BE IIb GenBank Acc: AF072725, L08065). At the same time, the amino acid sequences for different Class 2 branching enzymes each
5 have an identity of more than 60% with the amino acid sequence of branching enzyme IIb from maize (GenBank Acc: AF072725).

Vegetable or starch branching enzymes belong to the family of alpha-amylolytic enzymes (Svensson, 1994, Plant Molecular Biology 25, 141-157; Jespersen et al.,
10 1991, Biochem J. 280, 51-55) and, with regard to the amino acid sequence, have four conserved domains (Baba et al., 1991, Biochem. Biophys. Res. Commun. 181(1), 87-94; Kuriki et al., 1996, J. of Protein Chemistry 15(3), 305-313).

Structural predictions based on mathematical calculations derived from experimental
15 data such as protein crystal structures (Pfam: <http://hits.isb-sib.ch/cgi-bin/PFSCAN?>) show that all previously known branching enzymes from higher plants have two domains: an alpha-amylase domain and an iso-amylase domain. Here, the iso-amylase domain lies closer to the N-terminus of the protein than the alpha-amylase domain.

20 Plants are known, for example, which have a reduced activity of a Class 2 branching enzyme due to a mutation. These include the so-called "*amylose extender*" (*ae*) mutants from maize (Stindard et al., 1993, Plant Cell 5, 1555-1566; Boyer and Preiss, 1978, Biochem. Biophys. Res. Commun. 80, 169-175) and rice (Mizuno et al.,
25 1993, J. Biol. Chem. 268, 19084-19091), as well as the "*rugosus*" (*r*) mutation in pea (Smith, 1988, Planta 175, 270-279; Bhattacharyya et al., 1990, Cell 60, 115-122). All these mutants are distinguished by the fact that they synthesise a starch, which has an increased amylose content in comparison with starches from corresponding plants, which do not have this mutation.

30 Furthermore, genetically modified potato plants are described, in which the activity of a BE I (Class 1) branching enzyme (Kossmann et al., 1991, Mol Gen Genet 230, 39-44; Safford et al., 1998, Carbohydrate Polymers 35, 155-168), or the activity of a BEII

(Class 2) branching enzyme (Jobling et al., 1999, The Plant Journal 18), or the activity of a BEI and BEII branching enzyme (Schwall et al., 2000, Nature Biotechnology 18, 551- 554, Jobling et al., 2003, Nature Biotechnology 21, 77-80) are reduced.

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Previously, it has been possible to associate all vegetable branching enzymes to one or both of the classes described above. Plant cells or plants, which have a reduced activity of a branching enzyme, which cannot be associated with these classes, are unknown.

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The object of the present invention is therefore based on providing modified starches, new plant cells and/or plants, which synthesise such a modified starch, as well as means and methods for producing said plants.

15 This problem is solved by the embodiments described in the claims.

The present invention therefore relates to genetically modified plant cells and genetically modified plants, characterised in that the plant cells or plants have a reduced activity of at least one Class 3 branching enzyme in comparison with
20 corresponding wild type plant cells or wild type plants that have not been genetically modified.

A first aspect of the present invention relates to a plant cell or plant, which is genetically modified, wherein the genetic modification leads to the reduction of the
25 activity of at least one Class 3 branching enzyme in comparison with corresponding wild type plant cells or wild type plants that have not been genetically modified.

At the same time, the genetic modification can be any genetic modification, which leads to a reduction of the activity of at least one Class 3 branching enzyme in
30 comparison with corresponding wild type plant cells or wild type plants that have not been genetically modified.

In conjunction with the present invention, the term "wild type plant cell" means that the plant cells concerned were used as starting material for the manufacture of the plant cells according to the invention, i.e. their genetic information, apart from the introduced genetic modification, corresponds to that of a plant cell according to the invention.

In conjunction with the present invention, the term "wild type plant" means that the plants concerned were used as starting material for the manufacture of the plants according to the invention, i.e. their genetic information, apart from the introduced genetic modification, corresponds to that of a plant according to the invention.

In conjunction with the present invention, the term "corresponding" means that, in the comparison of several objects, the objects concerned that are compared with one another have been kept under the same conditions. In conjunction with the present invention, the term "corresponding" in conjunction with wild type plant cell or wild type plant means that the plant cells or plants, which are compared with one another, have been raised under the same cultivation conditions and that they have the same (cultivation) age.

In an embodiment of the present invention, the genetic modification of the plant cells according to the invention or the plants according to the invention is brought about by mutagenesis of one or more genes. The type of mutation is not important, as long as it leads to a reduction in the activity of a Class 3 branching enzyme.

In conjunction with the present invention, the term "mutagenesis" is to be understood to mean any type of introduced mutation, such as deletions, point mutations (nucleotide exchanges), insertions, inversions, gene conversions or chromosome translocations, for example.

Here, the mutation, which leads to the reduction of the activity of at least one endogenous Class 3 branching enzyme, can be produced by the use of chemical agencies or energy-rich radiation (e.g. x-rays, neutron radiation, gamma radiation or UV radiation).

Agencies, which can be used to produce chemically induced mutations, and the mutations resulting from the effect of the corresponding mutagens are, for example described in Ehrenberg and Husain, 1981, (Mutation Research 86, 1-113), Müller, 1972 (Biologisches Zentralblatt 91 (1), 31-48). The production of rice mutants using
5 gamma radiation, ethyl methane sulphonate (EMS), N-methyl-N-nitrosurea or sodium azide (NaN_3) is described, for example, in Jauhar and Siddiq (1999, Indian Journal of Genetics, 59 (1), 23-28), in Rao (1977, Cytologica 42, 443-450), Gupta and Sharma (1990, Oryza 27, 217-219) and Satoh and Omura (1981, Japanese Journal of Breeding 31 (3), 316-326). The production of wheat mutants using NaN_3 or maleic
10 hydrazide is described in Arora et al. (1992, Annals of Biology 8 (1), 65-69). An overview of the production of wheat mutants using different types of energy-rich radiation and chemical agencies is presented in Scarascia-Mugnozza et al. (1993, Mutation Breeding Review 10, 1-28). Svec et al. (1998, Cereal Research Communications 26 (4), 391-396) describes the use of N-ethyl-N-nitrosurea for
15 producing mutants in triticals. The use of MMS (methyl methane sulphonic acid) and gamma radiation for the production of millet mutants is described in Shashidhara et al. (1990, Journal of Maharashtra Agricultural Universities 15 (1), 20-23).

The manufacture of mutants in plant species, which mainly propagate vegetatively,
20 has been described, for example, for potatoes, which produce a modified starch (Hovenkamp-Hermelink et al. (1987, Theoretical and Applied Genetics 75, 217-221) and for mint with increased oil yield or modified oil quality (Dwivedi et al., 2000, Journal of Medicinal and Aromatic Plant Sciences 22, 460-463).

All these methods are basically suitable for manufacturing the plant cells according to
25 the invention and the plants according to the invention.

Mutations in the appropriate genes, in particular in genes coding a Class 3 branching enzyme, can be found with the help of methods known to the person skilled in the art. In particular, analyses based on hybridisations with probes (Southern Blot),
30 amplification by means of polymerase chain reaction (PCR), sequencing of related genomic sequences and the search for individual nucleotide exchanges can be used for this purpose. A method of identifying mutations based on hybridisation patterns is, for example, the search for restriction fragment length differences (Restriction

Fragment Length Polymorphism, RFLP) (Nam et al., 1989, The Plant Cell 1, 699-705; Leister and Dean, 1993, The Plant Journal 4 (4), 745-750). A method based on PCR is, for example, the analysis of amplified fragment length differences (Amplified Fragment Length Polymorphism, AFLP) (Castiglioni et al., 1998, Genetics 149, 2039-2056; Meksem et al., 2001, Molecular Genetics and Genomics 265, 207-214; Meyer et al., 1998, Molecular and General Genetics 259, 150-160). The use of amplified fragments cut with restriction endonucleases (Cleaved Amplified Polymorphic Sequences, CAPS) can be called upon for the identification of mutations (Konieczny and Ausubel, 1993, The Plant Journal 4, 403-410; Jarvis et al., 1994, Plant Molecular Biology 24, 685-687; Bachem et al., 1996, The Plant Journal 9 (5), 745-753). Methods for the determination of SNPs have been described by Qi et al. (2001, Nucleic Acids Research 29 (22), e116) Drenkard et al. (2000, Plant Physiology 124, 1483-1492) and Cho et al. (1999, Nature Genetics 23, 203-207) amongst others. Methods, which allow several plants to be investigated for mutations in certain genes in a short time, are particularly suitable. Such a method, so-called TILLING (Targeting Induced Local Lesions IN Genomes), has been described by McCallum et al. (2000, Plant Physiology 123, 439-442).

These methods are basically suitable for identifying plant cells according to the invention and plants according to the invention.

Hoogkamp et al. (2000, Potato Research 43, 179-189) have manufactured stable monoploid mutants starting from a potato mutant (*amf*), which was manufactured by means of chemical mutagens. These plants do not synthesise any more active enzyme for a starch synthesis connected to the starch grain (GBSS I) and therefore produce an amylose-free starch. The monoploid potato plants obtained can be used as starting material for further mutageneses in order to identify plants, which synthesise a starch with modified characteristics. The plant cells according to the invention and plants according to the invention, which produce a starch according to the invention, can be identified and isolated by appropriate methods.

The plant cells according to the invention and the plants according to the invention have a reduction of the activity of at least one Class 3 branching enzyme in

comparison with corresponding wild type plant cells that have not been genetically modified.

Here, within the framework of the present invention, the term "reduction of activity"
5 means a reduction in the expression of endogenous genes, which code Class 3 branching enzymes, and/or a reduction in the quantity of protein of a Class 3 branching enzyme in the plant cells and/or a reduction in the enzymatic activity of Class 3 branching enzymes in the plant cells.

10 The reduction in the expression can, for example, be determined by measuring the quantity of transcripts coding Class 3 branching enzyme, e.g. using Northern blot analysis or RT-PCR. Here, a reduction preferably means a reduction in the amount of transcripts in comparison with corresponding plant cells that have not been genetically modified by at least 50%, in particular by at least 70%, preferably by at
15 least 85% and particularly preferably by at least 95%.

The reduction in the amount of protein of a Class 3 branching enzyme, which results in a reduced activity of this protein in the plant cells concerned, can, for example, be determined by immunological methods such as Western blot analysis, ELISA
20 (Enzyme Linked Immuno Sorbent Assay) or RIA (Radio Immune Assay). Here, a reduction preferably means a reduction in the amount of Class 3 branching enzyme protein in comparison with corresponding plant cells that have not been genetically modified by at least 50%, in particular by at least 70%, preferably by at least 85% and particularly preferably by at least 95%.

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Within the framework of the present invention, the term "branching enzyme" (α -1,4-glucan: α -1,4- glucan 6-glycosyltransferase, E.C. 2.4.1.18) is understood to mean a protein, which catalyses a transglycosylation reaction, in which α -1,4 links of an α -1,4-glucan donor are hydrolysed and the thereby released α -1,4-glucan chains are
30 transferred to an α -1,4-glucan acceptor chain and, in doing so, are transformed into α -1,6-links. In particular, within the framework of the present invention, the term

"branching enzyme" is to be understood to mean a vegetable branching enzyme, i.e. a starch branching enzyme.

- The activity of a branching enzyme can be demonstrated, for example, with the help of native acrylamide gel electrophoresis. In doing so, proteins are first separated electrophoretically and, after incubation in buffers containing an activity, which synthesises linear α -1,4-glucan chains (e.g. starch phosphorylase a) and its substrate (e.g. glucose-6-phosphate), the corresponding gels are coloured with iodine (Kimihiro et al., 1980, Analytical Biochemistry 108, 16-24).
- Furthermore, branching enzymes in microbial organisms, such as the *E. coli* strain KV832 for example (Kiel et al., 1987 Mol. Gen. Genet 207: 294-301), which do not synthesise branched α -glucans, can be expressed. If an activity of a branching enzyme is introduced into the microbial organism due to the expression of a foreign gene in such strains (e.g. *E. coli* KV832), then the branching enzyme activity can be demonstrated by treating colonies of these organisms with iodine vapour, for example. Colonies, which synthesise linear α -1,4-glucans, turn blue in this test, while colonies, which synthesise branched glucans by expressing an additional enzymatic activity of a branching enzyme, turn reddish-brown after treating with iodine vapour. It is also possible to express proteins in phosphoglucomutase mutants of *E. coli* to identify a branching enzyme activity of appropriate proteins (Buettcher et al., 1999, Biochem. Biophys. Acta 1432, 406-412).

- A further possibility of demonstrating branching enzyme activity of proteins is the use of a reaction stimulated by phosphorylase a and the subsequent separation of the products by means of thin film chromatography (Almstrupp et al., 2000, Analytical Biochemistry 286, 297-300).

Branching enzyme activities can also be demonstrated with the help of the methods described in Guan and Preiss (1993, Plant Physiol. 102, 1269- 1273) and Kuriki et al. (1996, J. of Protein Chemistry 15, 305-313).

- In conjunction with the present invention, the term "Class 3 branching enzyme" is to be understood as a branching enzyme, which has a higher degree of identity with the amino acid sequence shown in SEQ ID NO 4 than with that of the branching enzyme BE I from maize (GenBank Acc: D11081) or with that of the branching enzyme BE IIb

from maize (GenBank Acc: AF072725). Preferably, the Class 3 branching enzyme comes from starch-storing plants, particularly preferably from plant species of the genus *Solanum*, especially preferably from *Solanum tuberosum*.

- 5 In a further embodiment of the present invention, amino acid sequences coding Class 3 branching enzymes have an identity of at least 60% with the sequence shown in SEQ ID NO 4, in particular of at least 70%, preferably of at least 80% and particularly preferably of at least 90% and especially preferably of at least 95%.
- 10 According to the invention, Class 3 branching enzymes have an iso-amylase domain (Pfam acc.: Pf02922) and an alpha-amylase domain (Pfam acc: Pf00128). According to the invention, the iso-amylase domain and the alpha-amylase domain in amino acid sequences coding branching enzymes are separated from one another by the presence of further amino acids, which do not belong to these two domains.
- 15 Class 3 branching enzymes according to the invention are distinguished by the fact that the iso-amylase domain is separated from the alpha-amylase domain by a greater number of amino acids than the iso-amylase domain and the alpha-amylase domain of Class 1 and 2 branching enzymes.
- Class 3 branching enzymes according to the invention are preferably distinguished
- 20 with regard to their amino acid sequence by the fact that they have at least 70, preferably at least 100, particularly preferably at least 130 and especially preferably at least 198 amino acids between the iso-amylase domain and the alpha-amylase domain. In a further embodiment of the present invention, in the case of an amino acid sequence coding a Class 3 branching enzyme, the C-terminal end of the iso-
- 25 amylase domain is separated from the N-terminal beginning of the alpha-amylase domain by 70 to 198, preferably by 100 to 198, particularly preferably by 130 to 198 and especially particularly preferably by 150 to 198 amino acids.

With the help of the Pfam database (Batemann et al., 2002, Nucleic Acids Research

30 30, 276-280; accessible via <http://www.sanger.ac.uk/Software/Pfam/>, <http://www.cgb.ki.se/Pfam/>; <http://pfam.jouy.inra.fr/> or <http://pfam.wustl.edu/>), it is possible for the person skilled in the art to determine whether amino acid sequences

already have known domains (e.g. an iso-amylase domain and/or an alpha-amylase domain).

- Pfam is a database put together by experts, which classifies amino acid sequences into so-called families. Here, the assignment of an amino acid sequence to a family is
- 5 carried out on the basis of so-called domains, which are to be looked upon as functional and structural components of proteins. A domain is defined as a structural unit or a repeatedly occurring amino acid sequence unit, which can occur in proteins with widely different functions. Along with information relating to the amino acid sequence of known proteins, further knowledge (e.g. evidence of the enzymatic
- 10 activity, crystal structure data) is also used for the assignment of a protein to a family. Each family is assigned a name and an "accession" number (e.g. Name: Isoamylase_N, acc: PF02922). A constituent part of each family in the Pfam database is, amongst other things, a so-called "seed alignment". The "seed alignment" contains the amino acid sequences of representative proteins of a family.
- 15 Starting from "seed alignments", a so-called profile HMM ("profile Hidden Markov Model"; overview article in: Durbin et al., "Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids", Cambridge University Press, 1998, ISBN 0-521-62041-4) is produced using the HMMER 2 software (freely available under <http://hmmer.wustl.edu/>). The HMMs produced have names and are stored in the
- 20 Pfam database specifically for the correspondingly assigned domains. In contrast to classical, multiple "alignments" (e.g. produced using the Clustal W program or the Blossum62 algorithm), HMMs are based on a valid statistical theory (Bayes theory of conditional probability, Markoff chains) and enable an interrogation sequence (query) to be assigned to a family based on the use of position-specific evaluation matrices.
- 25 This enables an assignment to be made even when there are considerable differences in the amino acid sequences between the interrogation sequence (query) and a comparison sequence (e.g. amino acid sequence entry in a database).

- The domain structure of the amino acid sequence concerned can be determined by
- 30 means of a comparison of the HMMs stored in the Pfam database with amino acid sequences, which are entered as a so-called interrogation sequence (query) (e.g. under <http://hits.isb-sib.ch/cgi-bin/PFSCAN?>).

In conjunction with the present invention, the term "iso-amylase domain" is to be understood to mean a Pfam iso-amylase domain (acc: Pf02922). At the same time, the HMM describing this Pfam iso-amylase domain is to be produced with the HMMER 2 [2.3.1] software, starting from a "seed alignment", which contains the amino acid sequences shown in Table 1. In conjunction with the present invention, the "seed alignment" is produced by means of the ClustalW program (Thompson et al., Nucleic Acids Research 22 (1994), 4673-4680; see below). The following settings must be chosen to produce the appropriate HMMs: Build Method of HMM: hmmbuild -F HMM_Is, hmmcalibrate -seed 0 HMM_Is; Gathering cutoff: 2.3 2.3; Trusted cutoff: 2.3 2.2; Noise cutoff: 2.1 2.1). Further information for producing the HMM of the Pfam iso-amylase domain (acc: Pf02922) is given in Table 3.

In conjunction with the present invention, the term "alpha-amylase domain" is to be understood to mean a Pfam alpha-amylase domain (acc: Pf00128). At the same time, the HMM describing this Pfam alpha-amylase domain is to be produced with the HMMER 2 [2.3.1] software, starting from a "seed alignment", which contains the amino acid sequences shown in Table 2. Here, the "seed alignment" is produced by means of HMM_simulated_annealing (<http://www.psc.edu/general/software/packages/hmmer/manual/node11.html#SECTION00321000000000000000>). The following settings must be chosen to produce the appropriate HMM: Build Method of HMM: hmmbuild -F HMM_Is, hmmcalibrate -seed 0 HMM_Is; Gathering cutoff: -82.0 -82.0; Trusted cutoff: -81.7 -81.7; Noise cutoff: -82.7 -82.7). Further information for producing the HMM of the Pfam alpha-amylase domain (acc: Pf00128) is given in Table 4.

In conjunction with the present invention, the term "Class 3 branching enzyme gene" is to be understood to mean a nucleic acid molecule (cDNA, DNA), which codes a Class 3 branching enzyme, preferably a Class 3 branching enzyme from starch-storing plants, particularly preferably from plant species of the genus *Solanum*, especially preferably from *Solanum tuberosum*.

A preferred embodiment of the present invention relates to a genetically modified plant cell according to the invention or a genetically modified plant according to the

invention, wherein the genetic modification consists in the introduction of at least one foreign nucleic acid molecule into the genome of the plant cell or into the genome of the plant.

- 5 In this context, the term "genetic modification" means the introduction of homologous and/or heterologous foreign nucleic acid molecules into the genome of a plant cell or into the genome of a plant, wherein said introduction of these molecules leads to a reduction of the activity of a Class 3 branching enzyme.

- The plant cells according to the invention or plants according to the invention are
10 modified with regard to their genetic information by the introduction of a foreign nucleic acid molecule. The presence or the expression of the foreign nucleic acid molecule leads to a phenotypic change. Here, "phenotypic" change means preferably a measurable change of one or more functions of the cells. For example, the genetically modified plant cells according to the invention and the genetically
15 modified plants according to the invention exhibit a reduction of the activity of a Class 3 branching enzyme due to the presence or on the expression of the introduced nucleic acid molecule.

- In conjunction with the present invention, the term "foreign nucleic acid molecule" is
20 understood to mean such a molecule that either does not occur naturally in the corresponding wild type plant cells that have not been genetically modified, or that does not occur naturally in the concrete spatial arrangement in wild type plant cells that have not been genetically modified, or that is localised at a place in the genome of the wild type plant cell at which it does not occur naturally. Preferably, the foreign
25 nucleic acid molecule is a recombinant molecule, which consists of different elements, the combination or specific spatial arrangement of which does not occur naturally in vegetable cells.

- In principle, the foreign nucleic acid molecule can be any nucleic acid molecule, which effects a reduction of the activity of a Class 3 branching enzyme in the plant
30 cell or plant.

In conjunction with the present invention, the term "genome" is to be understood to mean the totality of the genetic material present in a vegetable cell. It is known to the

person skilled in the art that, as well as the cell nucleus, other compartments (e.g. plastids, mitochondrions) also contain genetic material.

In a further embodiment, the plant cells according to the invention and the plants
5 according to the invention are characterised in that the foreign nucleic acid molecule codes a Class 3 branching enzyme, preferably a Class 3 branching enzyme from starch-storing plants, particularly preferably from plants of a species of the genus *Solanum*, especially preferably from *Solanum tuberosum*.

10 In a particularly preferred embodiment, the foreign nucleic acid molecule codes a Class 3 branching enzyme with the amino acid sequence specified in SEQ ID NO 4.

A large number of techniques are available for the introduction of DNA into a vegetable host cell. These techniques include the transformation of vegetable cells
15 with T-DNA using *Agrobacterium tumefaciens* or *Agrobacterium rhizogenes* as the transformation medium, the fusion of protoplasts, injection, the electroporation of DNA, the introduction of DNA by means of the biolistic approach as well as other possibilities.

The use of agrobacteria-mediated transformation of plant cells has been intensively
20 investigated and adequately described in EP 120516; Hoekema, IN: The Binary Plant Vector System Offsetdrukkerij Kanters B.V., Alblasterdam (1985), Chapter V; Fraley et al., Crit. Rev. Plant Sci. 4, 1-46 and by An et al. EMBO J. 4, (1985), 277-287. For the transformation of potato, see Rocha-Sosa et al., EMBO J. 8, (1989), 29-33, for example.

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The transformation of monocotyledonous plants by means of vectors based on agrobacterium transformation has also been described (Chan et al., Plant Mol. Biol. 22, (1993), 491-506; Hiei et al., Plant J. 6, (1994) 271-282; Deng et al, Science in China 33, (1990), 28-34; Wilmink et al., Plant Cell Reports 11, (1992), 76-80; May et al., Bio/Technology 13, (1995), 486-492; Conner and Domisse, Int. J. Plant Sci. 153
30 (1992), 550-555; Ritchie et al, Transgenic Res. 2, (1993), 252-265). An alternative system to the transformation of monocotyledonous plants is transformation by means of the biolistic approach (Wan and Lemaux, Plant Physiol. 104, (1994), 37-48; Vasil

et al., *Bio/Technology* 11 (1993), 1553-1558; Ritala et al., *Plant Mol. Biol.* 24, (1994), 317-325; Spencer et al., *Theor. Appl. Genet.* 79, (1990), 625-631), protoplast transformation, electroporation of partially permeabilised cells and the introduction of DNA by means of glass fibres. In particular, the transformation of maize has been
5 described in the literature many times (cf. e.g. WO95/06128, EP0513849, EP0465875, EP0292435; Fromm et al., *Biotechnology* 8, (1990), 833-844; Gordon-Kamm et al., *Plant Cell* 2, (1990), 603-618; Koziel et al., *Biotechnology* 11 (1993), 194-200; Moroc et al., *Theor. Appl. Genet.* 80, (1990), 721-726).

The successful transformation of other types of cereal has also already been
10 described, for example for barley (Wan and Lemaux, see above; Ritala et al., see above; Krens et al., *Nature* 296, (1982), 72-74) and for wheat (Nehra et al., *Plant J.* 5, (1994), 285-297). All the above methods are suitable within the framework of the present invention.

15 Amongst other things, the plant cells according to the invention and the plants according to the invention can be differentiated from wild type plant cells and wild type plants respectively in that they contain a foreign nucleic acid molecule, which does not occur naturally in wild type plant cells or wild type plants, or in that such a molecule is present integrated at a place in the genome of the plant cell according to
20 the invention or in the genome of the plant according to the invention at which it does not occur in wild type plant cells or wild type plants, i.e. in a different genomic environment. Furthermore, plant cells according to the invention and plants according to the invention of this type differ from wild type plant cells and wild type plants respectively in that they contain at least one copy of the foreign nucleic acid molecule
25 stably integrated within their genome; possibly in addition to naturally occurring copies of such a molecule in the wild type plant cells or wild type plants. If the foreign nucleic acid molecule(s) introduced into the plant cells according to the invention or into the plants according to the invention is (are) additional copies of molecules already occurring naturally in the wild type plant cells or wild type plants respectively,
30 then the plant cells according to the invention and the plants according to the invention can be differentiated from wild type plant cells or wild type plants respectively in particular in that this additional copy or these additional copies is (are) localised at places in the genome at which it does not occur (or they do not occur) in

wild type plant cells or wild type plants. This can be verified, for example, with the help of a Southern blot analysis.

- Furthermore, the plant cells according to the invention and the plants according to the invention can preferably be differentiated from wild type plant cells or wild type plants respectively by at least one of the following characteristics: If the foreign nucleic acid module that has been introduced is heterologous with respect to the plant cell or plant, then the plant cells according to the invention or plants according to the invention have transcripts of the introduced nucleic acid molecules. These can be verified, for example, by Northern blot analysis or by RT-PCR (Reverse Transcription Polymerase Chain Reaction). Plant cells according to the invention and plants according to the invention, which express an antisense and/or an RNAi transcript, can be verified, for example, with the help of specific nucleic acid probes, which are complimentary to the RNA (occurring naturally in the plant cell), which is coding for the protein.
- If the foreign nucleic acid module that has been introduced is homologous with respect to the plant cell or plant, the plant cells according to the invention or plants according to the invention can be differentiated from wild type plant cells or wild type plants respectively due to the additional expression of the introduced foreign nucleic acid molecule, for example. The plant cells according to the invention and the plants according to the invention preferably contain (sense and/or antisense) transcripts of the foreign nucleic acid molecules. This can be demonstrated by Northern blot analysis, for example, or with the help of so-called quantitative PCR.

In a special embodiment, the plant cells according to the invention and the plants according to the invention are transgenic plant cells or transgenic plants respectively.

In a further embodiment, the present invention relates to plant cells according to the invention and plants according to the invention wherein the foreign nucleic acid molecule is chosen from the group consisting of

- a) Nucleic acid molecules, which code a protein with the amino acid sequence given under Seq ID NO 4;

- b) Nucleic acid molecules, which code a protein, the amino acid sequence of which has an identity of at least 50% with the amino acid sequence given under SEQ ID NO: 4;
- 5 c) Nucleic acid molecules, which include the nucleotide sequence shown under Seq ID NO 3 or a complimentary sequence;
- d) Nucleic acid molecules, the nucleic acid sequence of which has an identity of at least 50% with the nucleic acid sequences described under a) or c);
- e) Nucleic acid molecules, which hybridise with at least one strand of the nucleic acid molecules described under a) or c) under stringent conditions;
- 10 f) Nucleic acid molecules, the nucleotide sequence of which deviates from the sequence of the nucleic acid molecules identified under a), b), c), d), e) or f) due to the degeneration of the genetic code; and
- g) Nucleic acid molecules, which represent fragments, allelic variants and/or derivatives of the nucleic acid molecules identified under a), b), c), d), e) or f).

15

A further embodiment of the present invention relates to plant cells according to the invention and plants according to the invention wherein the foreign nucleic acid molecule is chosen from the group consisting of

- 20 a) Nucleic acid molecules, which code at least one antisense RNA, which effects a reduction in the expression of at least one endogenous gene, which codes a Class 3 branching enzyme;
- b) Nucleic acid molecules, which by means of a co-suppression effect lead to the reduction in the expression of at least one endogenous gene, which codes a Class 3 branching enzyme;
- 25 c) Nucleic acid molecules, which code at least one ribozyme, which splits specific transcripts of at least one endogenous gene, which codes a Class 3 branching enzyme;
- d) Nucleic acid molecules, which simultaneously code at least one antisense RNA and at least one sense RNA, wherein the said antisense RNA and the
- 30 said sense RNA form a double-stranded RNA molecule, which effects a reduction in the expression of at least one endogenous gene, which codes a Class 3 branching enzyme (RNAi technology);

- 5 e) Nucleic acid molecules introduced by means of *in vivo* mutagenesis, which lead to a mutation or an insertion of a heterologous sequence in at least one endogenous gene coding a Class 3 branching enzyme, wherein the mutation or insertion effects a reduction in the expression of a gene coding a Class 3 branching enzyme or results in the synthesis of inactive Class 3 branching enzymes;
- f) Nucleic acid molecules, which code an antibody, wherein the antibody results in a reduction in the activity of a Class 3 branching enzyme due to the bonding to a Class 3 branching enzyme.
- 10 g) DNA molecules, which contain transposons, wherein the integration of these transposons leads to a mutation or an insertion in at least one endogenous gene coding a Class 3 branching enzyme, which effects a reduction in the expression of at least one gene coding a Class 3 branching enzyme, or results in the synthesis of inactive Class 3 branching enzymes; and/or
- 15 h) T-DNA molecules, which, due to insertion in at least one endogenous gene coding a Class 3 branching enzyme, effect a reduction in the expression of at least one gene coding a Class 3 branching enzyme, or result in the synthesis of inactive Class 3 branching enzyme.
- 20 The plant cells according to the invention and plants according to the invention can be manufactured by different methods known to the person skilled in the art. These include, for example, the expression of a corresponding antisense RNA or of a double-stranded RNA construct, the provision of molecules or vectors, which impart a cosuppression effect, the expression of a correspondingly constructed ribozyme that
- 25 splits specific transcripts, which code a Class 3 branching enzyme, or so-called "*in vivo* mutagenesis". Furthermore, the reduction of the Class 3 branching enzyme activity in plant cells and plants can also be brought about by the simultaneous expression of sense and antisense RNA molecules of the respective target gene to be repressed, preferably of the Class 3 branching enzyme gene.
- 30 In addition to this, it is known that *in planta* the formation of double-stranded RNA molecules of promoter sequences can lead *in trans* to methylation and transcriptional inactivation of homologous copies of this promoter (Mette et al., EMBO J. 19, (2000), 5194-5201).

A further possible way in which to reduce the enzymatic activity of proteins in plant cells or plants is the so-called immunomodulation method. It is known that an *in planta* expression of antibodies, which specifically recognise a vegetable protein, results in a reduction of the activity of the proteins concerned in appropriate plant cells due to the formation of a protein antibody complex (Conrad and Manteufel, Trends in Plant Science 6, (2001), 399-402; De Jaeger et al., Plant Molecular Biology 43, (2000), 419-428; Jobling et al., Nature Biotechnology 21, (2003), 77-80).

All these methods are based on the introduction of a foreign or of several foreign nucleic acid molecules into the genome of plant cells or plants and are therefore basically suitable for manufacturing plant cells according to the invention and plants according to the invention.

For inhibiting the expression of genes by means of antisense or cosuppression technology, a DNA molecule can be used, for example, which includes the whole coding sequence for a Class 3 branching enzyme, including any existing flanking sequences, as well as DNA molecules, which include only parts of the coding sequence, whereby these parts must be long enough to produce an antisense effect or a cosuppression effect respectively in the cells. In general, sequences up to a minimum length of 21 bp, preferably a minimum length of at least 100 bp, particularly preferably of at least 500 bp are suitable. For example, the DNA molecules have a length of 21-100 bp, preferably of 100-500 bp, particularly preferably over 500 bp.

The use of DNA sequences, which have a high degree of identity with the endogenous sequences occurring in the plant cells and which code Class 3 branching enzymes, is also suitable for antisense or cosuppression approaches. The minimum identity should be greater than ca. 65%, preferably greater than 80%. The use of sequences with identities of at least 90%, in particular between 95% and 100%, is to be preferred. The meaning of the term "identity" will be defined elsewhere.

Furthermore, the use of introns, i.e. of non-coding areas of genes, which code for Class 3 branching enzymes, is also conceivable for achieving an antisense or a cosuppression effect.

The use of intron sequences for inhibiting the gene expression of genes, which code for starch biosynthesis proteins, has been described in the international patent applications WO97/04112, WO97/04113, WO98/37213, WO98/37214.

- 5 The person skilled in the art knows how to achieve an antisense and a cosuppression effect. For example, the method of cosuppression inhibition has been described in Jorgensen (Trends Biotechnol. 8 (1990), 340-344), Niebel et al., (Curr. Top. Microbiol. Immunol. 197 (1995), 91-103), Flavell et al. (Curr. Top. Microbiol. Immunol. 197 (1995), 43-46), Palaqui and Vaucheret (Plant. Mol. Biol. 29 (1995), 149-159), Vaucheret et al., (Mol. Gen. Genet. 248 (1995), 311-317), de Borne et al. (Mol. Gen. Genet. 243 (1994), 613-621).

- The expression of ribozymes for reducing the activity of particular enzymes in cells is also known to the person skilled in the art, and is described, for example, in EP-B1 15 0321201. The expression of ribozymes in vegetable cells has been described, for example, in Feyter et al. (Mol. Gen. Genet. 250, (1996), 329-338).

- The reduction of the activity of a Class 3 branching enzyme in plant cells according to the invention and plants according to the invention can also be brought about by the 20 simultaneous expression of sense and antisense RNA molecules (RNAi technology) of the respective target gene to be repressed, preferably of the Class 3 branching enzyme gene.

- This can be achieved, for example, by the use of chimeric constructs, which contain "inverted repeats" of the respective target gene or parts of the target gene. In this 25 case, the generic constructs code for sense and antisense RNA molecules of the respective target gene. Sense and antisense RNA are synthesised simultaneously *in planta* as an RNA molecule, wherein sense and antisense RNA are separated from one another by a spacer, and are able to form a double-stranded RNA molecule.

- It has been shown that the introduction of inverted repeat DNA constructs into the 30 genome of plant cells or plants is a very effective method of repressing the genes corresponding to the inverted repeat DNA constructs (Waterhouse et al., Proc. Natl. Acad. Sci. USA 95, (1998), 13959-13964; Wang and Waterhouse, Plant Mol. Biol. 43, (2000), 67-82; Singh et al., Biochemical Society Transactions Vol. 28 part 6

(2000), 925- 927; Liu et al., Biochemical Society Transactions Vol. 28 part 6 (2000), 927-929; Smith et al., (Nature 407, (2000), 319-320; international patent application WO99/53050 A1). Sense and antisense sequences of the target gene or the target genes can also be expressed separately from one another by means of similar or
5 different promoters (Nap, J-P. et al, 6th International Congress of Plant Molecular Biology, Quebec, 18th-24th June, 2000; Poster S7-27, Presentation Session S7).

The reduction of the activity of a Class 3 branching enzyme in plant cells according to the invention or plants according to the invention can therefore also be achieved by
10 producing double-stranded RNA molecules. In this regard, "inverted repeats" of DNA molecules of Class 3 branching enzyme genes or cDNAs are preferably introduced into the genome of plants, wherein the DNA molecules (Class 3 branching enzyme gene or cDNA or fragments of this gene or cDNA) to be transcribed are under the control of a promoter, which controls the expression of said DNA molecules.

15

In addition to this, it is known that the formation of double-stranded RNA molecules from promoter DNA molecules in plants *in trans* can lead to methylation and transcriptional inactivation of homologous copies of these promoters, which are to be referred to in the following as target promoters (Mette et al., EMBO J. 19, (2000),
20 5194-5201).

It is therefore possible to reduce the gene expression of a particular target gene (e.g. branching enzyme Class 3 gene), which is naturally under the control of this target promoter, by deactivating the target promoter.

This means that, in this case, the DNA molecules, which include the target promoters
25 of the genes to be repressed (target genes), in contrast to the original function of promoters in plants, are not used as control elements for the expression of genes or cDNAs, but are themselves used as transcribable DNA molecules.

For the production of double-stranded target promoter RNA molecules *in planta*, which can occur there as RNA hairpin molecules, constructs are preferably used,
30 which contain the "inverted repeats" of the target promoter DNA molecules, wherein the target promoter DNA molecules are under the control of a promoter, which controls the gene expression of said target promoter DNA molecules. These constructs are subsequently introduced into the genome of plants. The expression of

the "inverted repeats" of said target promoter DNA molecules *in planta* leads to the formation of double-stranded target promoter RNA molecules (Mette et al., EMBO J. 19, (2000), 5194-5201). The target promoter can be inactivated by this means.

The reduction of the activity of a Class 3 branching enzyme in plant cells according to the invention and plants according to the invention can therefore also be achieved by the production of double-stranded RNA molecules of promoter sequences of Class 3 branching enzyme genes. In this regard, "inverted repeats" of promoter DNA molecules of Class 3 branching enzyme genes are preferably introduced into the genome of plants, wherein the target promoter DNA molecules (promoter of a Class 3 branching enzyme gene) to be transcribed are under the control of a promoter, which controls the expression of said target promoter DNA molecules.

For inhibiting the expression of genes by means of the simultaneous expression of sense and antisense RNA molecules (RNAi technology), a DNA molecule can be used, for example, which includes the whole coding sequence for a Class 3 branching enzyme, including any existing flanking sequences, as well as DNA molecules, which include only parts of the coding sequence, whereby these parts must be long enough to produce a so-called RNAi effect in the cells. In general, sequences with a minimum length of 40 bp, preferably a minimum length of at least 100 bp, particularly preferably of at least 500 bp are suitable. For example, the DNA molecules have a length of 21-100 bp, preferably of 100-500 bp.

The use of DNA sequences, which have a high degree of identity with the endogenous sequences occurring in the plant cells and which code Class 3 branching enzymes, is also suitable for the simultaneous expression of sense and antisense RNA molecules (RNAi technology). The minimum identity should be greater than ca. 65%, preferably greater than 80%. The use of sequences with identities of at least 90%, in particular between 95% and 100%, is to be particularly preferred.

30

Furthermore, the reduction of the activity of a Class 3 branching enzyme in plant cells according to the invention and plants according to the invention can also be achieved by so-called "in vivo mutagenesis", in which a hybrid RNA-DNA oligonucleotide

("Chimeroplast") is introduced into plant cells (Kipp, P.B. et al., Poster Session at the "5th International Congress of Plant Molecular Biology, 21st-27th September 1997, Singapore; R. A. Dixon and C.J. Arntzen, meeting report on "Metabolic Engineering in Transgenic Plants", Keystone Symposia, Copper Mountain, CO, USA, TIBTECH 5 15, (1997), 441-447; international patent application WO 9515972; Kren et al., Hepatology 25, (1997), 1462-1468; Cole-Strauss et al., Science 273, (1996), 1386-1389; Beetham et al., 1999, PNAS 96, 8774-8778).

A part of the DNA components of the RNA-DNA oligonucleotide is homologous to a nucleic acid sequence of an endogenous Class 3 branching enzyme gene, but, in 10 comparison with the nucleic acid sequence of a Class 3 branching enzyme gene, it has a mutation or contains a heterologous region, which is surrounded by the homologous regions.

By base pairing of the homologous regions of the RNA-DNA oligonucleotide and the endogenous nucleic acid molecule followed by homologous recombination, the 15 mutation or heterologous region contained in the DNA components of the RNA-DNA oligonucleotide can be transferred into the genome of a plant cell. This leads to the reduction of the activity of one or more Class 3 branching enzymes.

The person skilled in the art knows that he can achieve the activity of Class 3 20 branching enzymes by the expression of non-functional derivatives, in particular transdominant mutants, of such proteins, and/or by the expression of antagonists/inhibitors of such proteins.

Antagonist/inhibitors of such proteins include, for example, antibodies, antibody fragments or molecules with similar bonding characteristics. For example, a 25 cytoplasmatic scFv antibody has been used to modulate the activity of the phytochrome A protein in genetically modified tobacco plants (Owen, Bio/Technology 10 (1992), 790-4; Review: Franken, E, Teuschel, U. and Hain, R., Current Opinion in Biotechnology 8, (1997), 411-416; Whitelam, Trends Plant Sci. 1 (1996), 268-272; Conrad and Manteufel, Trends in Plant Science 6, (2001), 399-402; De Jaeger et al., 30 Plant Molecular Biology 43, (2000), 419-428). The reduction of the activity of a branching enzyme in potato plants by expressing a specific antibody has been described by Jobling et al. (Nature Biotechnology 21, (2003), 77-80). Here, the

antibody was provided with a plastidial target sequence so that the inhibition of proteins localised in plastids was guaranteed.

In conjunction with the present invention, plant cells and plants according to the invention can also be manufactured by the use of so-called insertion mutagenesis (overview article: Thorneycroft et al., 2001, Journal of experimental Botany 52 (361), 1593-1601). Insertion mutagenesis is to be understood to mean particularly the insertion of transposons or so-called transfer DNA (T-DNA) into a gene coding for a Class 3 branching enzyme, whereby, as a result of which, the activity of a Class 3 branching enzyme in the cell concerned is reduced.

The transposons can be both those that occur naturally in the cell (endogenous transposons) and also those that do not occur naturally in said cell but are introduced into the cell (heterologous transposons) by means of genetic engineering methods, such as transformation of the cell, for example. Changing the expression of genes by means of transposons is known to the person skilled in the art. An overview of the use of endogenous and heterologous transposons as tools in plant biotechnology is presented in Ramachandran and Sundaresan (2001, Plant Physiology and Biochemistry 39, 234-252). The possibility of identifying mutants in which specific genes have been inactivated by transposon insertion mutagenesis is presented in an overview by Maes et al. (1999, Trends in Plant Science 4 (3), 90-96). The production of rice mutants with the help of endogenous transposons is described by Hirochika (2001, Current Opinion in Plant Biology 4, 118-122). The identification of maize genes with the help of endogenous retrotransposons is presented, for example, by Hanley et al. (2000, The Plant Journal 22 (4), 557-566). The possibility of manufacturing mutants with the help of retrotransposons and methods of identifying mutants are described by Kumar and Hirochika (2001, Trends in Plant Science 6 (3), 127-134). The activity of technological transposons in different species has been described both for dicotyledonous and for monocotyledonous plants: e.g. for rice (Greco et al., 2001, Plant Physiology 125, 1175-1177; Liu et al., 1999, Molecular and General Genetics 262, 413-420; Hiroyuki et al., 1999, The Plant Journal 19 (5), 605-613; Jeon und Gynheung, 2001, Plant Science 161, 211-219), barley (2000, Koprek et al., The Plant Journal 24 (2), 253-263) *Arabidopsis thaliana* (Aarts et al., 1993,

Nature 363, 715-717, Schmidt und Willmitzer, 1989, Molecular and General Genetics 220, 17-24; Altmann et al., 1992, Theoretical and Applied Genetics 84, 371-383; Tissier et al., 1999, The Plant Cell 11, 1841-1852), tomato (Belzile und Yoder, 1992, The Plant Journal 2 (2), 173-179) and potato (Frey et al., 1989, Molecular and
5 General Genetics 217, 172-177; Knapp et al., 1988, Molecular and General Genetics 213, 285-290).

Basically, the plant cells according to the invention and the plants according to the invention can be manufactured both with the help of homologous and heterologous
10 transposons, whereby the use of homologous transposons is also to be understood to mean those, which are naturally present in the corresponding wild type plant genome.

T-DNA insertion mutagenesis is based on the fact that certain sections (T-DNA) of Ti
15 plasmids from *Agrobacterium* can integrate into the genome of vegetable cells. The place of integration in the vegetable chromosome is not defined, but can take place at any point. If the T-DNA integrates into a part of the chromosome, which constitutes a gene function, then this can lead to a change in the gene expression and thus also to a change in the activity of a protein coded by the gene concerned. In particular, the
20 integration of a T-DNA into the coded area of a protein often leads to the corresponding protein no longer being able to be synthesised at all, or no longer synthesised in active form, by the cell concerned. The use of T-DNA insertions for producing mutants is described, for example, for *Arabidopsis thaliana* (Krysan et al., 1999, The Plant Cell 11, 2283-2290; Atipiroz-Leehan and Feldmann, 1997, Trends in
25 genetics 13 (4), 152-156; Parinov and Sundaresan, 2000, Current Opinion in Biotechnology 11, 157-161) and rice (Jeon and An, 2001, Plant Science 161, 211-219; Jeon et al., 2000, The Plant Journal 22 (6), 561-570). Methods for identifying mutants, which have been produced with the help of T-DNA insertion mutagenesis, are described, amongst others, by Young et al., (2001, Plant Physiology 125, 513-
30 518), Parinov et al. (1999, The Plant cell 11, 2263-2270), Thorneycroft et al. (2001, Journal of Experimental Botany 52, 1593-1601), and McKinney et al. (1995, The Plant Journal 8 (4), 613-622).

T-DNA mutagenesis is basically suitable for the production of the plant cells and plants according to the invention, which have a reduced activity of a Class 3 branching enzyme.

- 5 Surprisingly, it has been found that plant cells according to the invention and plants according to the invention synthesise a modified starch in comparison with starch of corresponding wild type plant cells or wild type plants that have not been genetically modified.
- 10 The plant cells according to the invention and plants according to the invention synthesise a modified starch, which in its physical-chemical characteristics, in particular the amylose content or the amylose/amylopectin ratio, the degree of branching, the average chain length, the side chain distribution, the viscosity behaviour, the gelling strength, the starch grain size and/or the starch grain
- 15 morphology, is changed in comparison with the synthesised starch in wild type plant cells or plants, so that this is better suited for special applications.

- It was surprisingly found that plant cells or plants of the invention synthesize a modified starch having decreased phosphate content. So far known plants with a
- 20 reduced activity of a branching enzyme (Class 1 and/or Class 2) did show an increased phosphate content.

- The present invention therefore also includes plant cells according to the invention and plants according to the invention, which synthesise a modified starch.
- 25

- In a preferred embodiment of the invention, the plant cells according to the invention or the plant according to the invention synthesize a starch with a decreased phosphate content in comparison with corresponding starch isolated from wild type plant cells or wild type plants that have not been genetically modified. Preferably the
- 30 plant cells according to the invention or the plants according to the invention synthesize a starch having a total phosphate content that is decreased by at least 10%, more preferably by at least 15% and particular preferably by at least 20% in comparison with starch isolated from corresponding wild type plant cells or wild type

plants that have not been genetically modified. Especially preferably the total phosphate content of starch isolated from plant cells of the invention or plants of the invention is decreased by 14% to 22% in comparison with starch isolated from corresponding wild type plant cells or wild type plants that have not been genetically modified.

In respect with C-6-phosphate content the plant cells according to the invention or the plants according to the invention synthesize a starch having a C-6-phosphate content that is decreased by at least 15%, more preferably by at least 19% and particular preferably by at least 25% in comparison with starch isolated from corresponding wild type plant cells or wild type plants that have not been genetically modified. Especially preferably the C-6-phosphate content of starch isolated from plant cells of the invention or plants of the invention is decreased by 15%% to 27% in comparison with starch isolated from corresponding wild type plant cells or wild type plants that have not been genetically modified.

Methods for the determination of total phosphate or C-6-phosphate content in starches are well known by a person skilled in the art. Preferred methods for the determination of total or C-6-phosphate content in starches to be used in combination with the present invention are described below in the section "general methods" (Starch analysis, e). Analysis of the side-chain distribution of the amylopectin by means of ion-exchange chromatography).

In a further preferred embodiment of the invention, the plant cells according to the invention or the plants according to the invention synthesize a starch which has an altered viscosity behaviour in comparison with starch isolated from corresponding wild type plant cells or wild type plants that have not been genetically modified. Plant cells of the invention or plants of the invention synthesize a starch which has a decreased maximum viscosity, a decreased minimum viscosity and/or a decreased final viscosity in comparison with starch isolated from corresponding wild type plant cells or wild type plants that have not been genetically modified.

The maximum viscosity of starch isolated from plant cells of the invention or plants of the invention is preferably decreased by at least 8% and more preferably by at least

16% in comparison with starch isolated from corresponding wild type plant cells or wild type plants that have not been genetically modified. Especially preferably the maximum viscosity of starch isolated from plant cells of the invention or plants of the invention is decreased by 8% to 16%_in comparison with starch isolated from
5 corresponding wild type plant cells or wild type plants that have not been genetically modified.

The minimum viscosity of starch isolated from plant cells of the invention or plants of the invention is preferably decreased by at least 10%, more preferably by at least 15% and particularly preferably by at least 25% in comparison with starch isolated
10 from corresponding wild type plant cells or wild type plants that have not been genetically modified. Especially preferably the minimum viscosity of starch isolated from plant cells of the invention or plants of the invention is decreased by 15% to 25% in comparison with starch isolated from corresponding wild type plant cells or wild type plants that have not been genetically modified.

15 The final viscosity of starch isolated from plant cells of the invention or plants of the invention is preferably decreased by at least 5% and more preferably by at least 10% in comparison with starch isolated from corresponding wild type plant cells or wild type plants that have not been genetically modified. Particularly preferably the minimum viscosity of starch isolated from plant cells of the invention or plants of the
20 invention is decreased by 5% to 10% in comparison with starch isolated from corresponding wild type plant cells or wild type plants that have not been genetically modified.

It has further been found, that starch isolated from plant cells of the invention or
25 plants of the invention shows an increased gelling strength in comparison with starch isolated from corresponding wild type plant cells or wild type plants that have not been genetically modified.

The present invention therefore also comprises plant cells of the invention or plants
30 of the invention that synthesize a starch with an increased gel strength in comparison with starch isolated from corresponding wild type plant cells or wild type plants that have not been genetically modified. Preferably plant cells of the invention or plants of the invention synthesize a starch which shows a gel strength which is increased by at

least 20%, more preferably by at least 30% and particular preferably by at least 35% in comparison with starch isolated from corresponding wild type plant cells or wild type plants that have not been genetically modified. Especially preferably the gel strength of starch isolated from plant cells of the invention or plants of the invention is
5 increased by 27% to 38% in comparison with starch isolated from corresponding wild type plant cells or wild type plants that have not been genetically modified.

Methods for the determination of viscosity behaviour or gelling properties of starches are well known by a person skilled in the art. Preferred methods for the determination
10 of viscosity behaviour or gelling properties of starches to be used in combination with the present invention are described below in the section "general methods".

Furthermore it was surprisingly found that starch, isolated from plant cells of the invention or plants of the invention shows an altered side chain distribution pattern in
15 the amylopectin fraction in comparison with the amylopectin fraction from starch isolated from corresponding wild type plant cells or wild type plants that have not been genetically modified.

In a further embodiment of the invention, plant cells according to the invention or the
20 plants according to the invention synthesize a starch with an altered short-side-chain distribution pattern in the amylopectin fraction in comparison with the amylopectin fraction from starch isolated from corresponding wild type plant cells or wild type plants that have not been genetically modified. Preferably plant cells according to the invention or the plants according to the invention synthesize a starch wherein the
25 short-side-chains in the amylopectin fraction having a degree of polymerization (DP) of 6 and/or a DP of 7 is increased in comparison with the amylopectin fraction from starch isolated from corresponding wild type plant cells or wild type plants that have not been genetically modified. More preferably the amylopectin fraction of starch isolated from plant cells according to the invention or plants according to the
30 invention synthesize a starch wherein short-side-chains with a DP 6 is increased by at least 15%, particularly preferably by at least 20%, especially particularly by at least 25% and/or the short-side-chains with a DP 7 are increased by at least 2%, particularly preferably by at least 4%, especially preferably by at least 8% in

comparison with the amylopectin fraction from starch isolated from corresponding wild type plant cells or wild type plants that have not been genetically modified.

In a further preferred embodiment of the invention the plant cells according to the invention or the plants according to the invention synthesize a starch wherein the
5 short-side-chains of DP 6 in the amylopectin fraction is increased by 17% to 29% and/or the side chains of DP 7 in the amylopectin fraction is increased by 2% to 9% in comparison with the amylopectin fraction from starch isolated from corresponding wild type plant cells or wild type plants that have not been genetically modified.

10 In conjunction with the present invention, the term "short-side-chain" shall mean alpha-1,6-linked side-chains in the starch molecule having a degree of polymerization between DP 6 and DP 34.

Methods for the quantification of short-side-chains having a specified DP in the
15 amylopectin fraction are well known by the person skilled in the art. Preferred methods for the quantification of side-chains having a specified DP, suitable to be used in combination with the present invention are described below in the section "general methods (Analysis of the side-chain distribution of the amylopectin by means of ion-exchange chromatography).

20

Furthermore it was found that the amylopectin fraction of starch, isolated from the plant cells according to the invention or the plants according to the invention shows an altered total-side-chain distribution.

25 Therefore, further embodiments of the present invention are the plant cells according to the invention or the plants according to the invention which synthesize a starch wherein the groups of total-side-chains in the amylopectin fraction characterized by the following ranges:

- a) DP up to 11,
- 30 b) DP 12 to DP 19,
- c) DP 20 to DP 25 and/or
- d) DP 26 to DP 31

is/are increased and/or the groups of total-side-chains in the amylopectin fraction characterized by the following ranges:

- a) DP 38 to DP 43
- b) DP 44 to DP 49
- 5 c) DP 50 to DP 56
- d) DP 57 to DP 62 and/or
- e) DP 63 to DP 123

is/are decreased in comparison with the amylopectin fraction from starch isolated from corresponding wild type plant cells or wild type plants that have not been
10 genetically modified.

In conjunction with the present invention, the term "total-side-chains" shall mean alpha-1,6-linked side-chains in the starch molecule having a degree of polymerization up to DP 123. A group of total-side-chains consists of all side-chains spanning a
15 defined DP range (e.g. DP up to 11, DP 12 to DP 19, DP 20 to DP 25, DP 26 to DP 31, DP 38 to DP 43, DP 44 to DP 49, DP 50 to DP 56, DP 57 to DP 62, DP 63 to DP 123).

Methods for the quantification of groups of total-side-chains spanning ranges of side-
20 chains with a specified DP in the amylopectin fraction are well known by the person skilled in the art. Preferred methods for the quantification groups of total-side-chains, suitable to be used in combination with the present invention are described below in example 5d).

25 Further embodiments of the invention are the plant cells according to the invention or the plants according to the invention which synthesize a starch having a decreased peak onset Temperature (T_0), a decreased peak temperature (T_{Peak}) and an increased delta H (ΔH) when analyzed by differential scanning calorimetric (DSC) in comparison to starch isolated from corresponding wild type plant cells or wild type
30 plants that have not been genetically modified.

Methods for the analysis of starch by DSC are well known by a person skilled in the art. Preferred Methods for DSC analysis suitable to be used in combination with the

present invention are described below in the section "general methods" (DSC-analysis („Differential Scanning Calorimetry“).

Furthermore, genetically modified plants, which contain the plant cells according to
5 the invention, are also the subject matter of the invention. Plants of this type can be produced from plant cells according to the invention by regeneration.

In principle, the plants according to the invention can be plants of any plant species, i.e. both monocotyledonous and dicotyledonous plants. Preferably they are useful plants, i.e. plants, which are cultivated by people for the purposes of food or for
10 technical, in particular industrial purposes.

In a further preferred embodiment, the plant according to the invention is a starch-storing plant.

15 In a further preferred embodiment, the present invention relates to starch-storing plants according to the invention of the genus *Solanum*, in particular *Solanum tuberosum*.

The term "starch-storing plants" includes all plants with starch-storing plant parts
20 such as, for example, maize, rice, wheat, rye, oat, barley, cassava, potato, sago, mung bean, pea or sorghum. Preferred starch-storing plant parts are, for example, tubers, storage roots and grains containing an endosperm; tubers are particularly preferred.

25 In conjunction with the present invention, the term "potato plant" or "potato" means plant species of the genus *Solanum*, in particular tuber-producing species of the genus *Solanum* and especially *Solanum tuberosum*.

The present invention also relates to propagation material of plants according to the
30 invention containing a plant cell according to the invention.

Here, the term "propagation material" includes those constituents of the plant that are suitable for producing offspring by vegetative or sexual means. Cuttings, callus

cultures, rhizomes or tubers, for example, are suitable for vegetative propagation. Other propagation material includes, for example, fruits, seeds, seedlings, protoplasts, cell cultures, etc. Preferably, the propagation material is seeds and particularly preferably tubers.

5

In a further embodiment, the present invention relates to harvestable plant parts of plants according to the invention such as fruits, storage roots, roots, blooms, buds, shoots or stems, preferably seeds or tubers, wherein these harvestable parts contain at least one plant cell according to the invention.

10

Furthermore, the present invention also relates to a method for the manufacture of a plant according to the invention, wherein

- a) a plant cell is genetically modified, whereby the genetic modification leads to the reduction of the activity of a Class 3 vegetable branching enzyme in comparison with corresponding wild type plant cells that have not been genetically modified;
- 15 b) a plant is regenerated from plant cells from Step a); and
- c) if necessary, further plants are produced with the help of the plants according to Step b).

20

The genetic modification introduced into the plant cell according to Step a) can basically be any type of genetic modification, which leads to the reduction of the activity of a Class 3 branching enzyme.

- 25 The regeneration of the plants according to Step (b) can be carried out using methods known to the person skilled in the art (e.g. described in "Plant Cell Culture Protocols", 1999, ed. by R.D. Hall, Humana Press, ISBN 0-89603-549-2).

The production of further plants according to Step (c) of the method according to the invention can be carried out, for example, by vegetative propagation (for example using cuttings, tubers or by means of callus culture and regeneration of whole plants) or by sexual propagation. Here, sexual propagation preferably takes place under

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controlled conditions, i.e. selected plants with particular characteristics are crossed and propagated with one another.

5 In a preferred embodiment of the method according to the invention, the genetic modification consists in the introduction of a foreign nucleic acid molecule into the genome of the plant cell, wherein the presence or the expression of said foreign nucleic acid molecule leads to a reduced activity of a Class 3 branching enzyme in the cell.

10 The statements made in conjunction with plant cells according to the invention and plants according to the invention apply with regard to the "introduction of a foreign nucleic acid molecule".

15 In a further preferred embodiment, the method according to the invention is used for producing potato plants according to the invention.

In a further preferred embodiment of the method according to the invention, the foreign nucleic acid molecule is chosen from the group consisting of

- 20 a) Nucleic acid molecules, which code a protein with the amino acid sequence given under Seq ID NO 4;
- b) Nucleic acid molecules, which code a protein, the amino acid sequence of which has an identity of at least 50% with the amino acid sequence given under SEQ ID NO: 4;
- 25 c) Nucleic acid molecules, which include the nucleotide sequence shown under Seq ID NO. 3 or a complimentary sequence;
- d) Nucleic acid molecules, the nucleic acid sequence of which has an identity of at least 50% with the nucleic acid sequences described under a) or c);
- e) Nucleic acid molecules, which hybridise with at least one strand of the nucleic acid molecules described under a) or c) under stringent conditions;
- 30 f) Nucleic acid molecules, the nucleotide sequence of which deviates from the sequence of the nucleic acid molecules identified under a), b), c), d), e) or f) due to the degeneration of the genetic code; and

- g) Nucleic acid molecules, which represent fragments, allelic variants and/or derivatives of the nucleic acid molecules identified under a), b), c), d), e) or f).

In a further preferred embodiment of the method according to the invention, the
5 foreign nucleic acid molecule is chosen from the group consisting of

- a) Nucleic acid molecules, which code at least one antisense RNA, which effects a reduction in the expression of at least one endogenous gene, which codes a Class 3 branching enzyme;
- 10 b) Nucleic acid molecules, which by means of a co-suppression effect lead to the reduction in the expression of at least one endogenous gene, which codes a Class 3 branching enzyme;
- c) Nucleic acid molecules, which code at least one ribozyme, which splits specific transcripts of at least one endogenous gene, which codes a Class 3 branching enzyme;
- 15 d) Nucleic acid molecules, which simultaneously code at least one antisense RNA and at least one sense RNA, wherein the said antisense RNA and the said sense RNA form a double-stranded RNA molecule, which effects a reduction in the expression of at least one endogenous gene, which codes a Class 3 branching enzyme (RNAi technology);
- 20 e) Nucleic acid molecules introduced by means of in vivo mutagenesis, which lead to a mutation or an insertion of a heterologous sequence in at least one endogenous gene coding a Class 3 branching enzyme, wherein the mutation or insertion effects a reduction in the expression of a gene coding a Class 3 branching enzyme or results in the synthesis of inactive Class 3 branching enzymes;
- 25 f) Nucleic acid molecules, which code an antibody, wherein the antibody results in a reduction in the activity of a Class 3 branching enzyme due to the bonding to a Class 3 branching enzyme.
- 30 g) Nucleic acid molecules, which contain transposons, wherein the integration of these transposons leads to a mutation or an insertion in at least one endogenous gene coding a Class 3 branching enzyme, which effects a reduction in the expression of at least one gene coding a Class 3 branching

enzyme, or results in the synthesis of inactive Class 3 branching enzymes; and/or

- h) T-DNA molecules, which, due to insertion in at least one endogenous gene coding a Class 3 branching enzyme, effect a reduction in the expression of at least one gene coding a Class 3 branching enzyme, or result in the synthesis of inactive Class 3 branching enzyme.

In a further embodiment of the method according to the invention, the genetically modified plants according to the invention synthesise a modified starch in comparison with corresponding wild type plants that have not been genetically modified.

In a further embodiment of the method according to the invention, the method according to the invention is used to manufacture plants according to the invention.

The present invention also relates to the plants obtainable by the method according to the invention.

It is also an object of the present invention to provide means such as DNA molecules, for example, for the production of plant cells according to the invention and plants according to the invention, which synthesise a modified starch in comparison with modified wild type plant cells or wild type plants that have not been genetically modified.

The present invention therefore also relates to nucleic acid molecules coding for a protein with the enzymatic activity of a Class 3 branching enzyme, chosen from the group consisting of

- a) Nucleic acid molecules, which code a protein with the amino acid sequence given under Seq ID NO 4;
- b) Nucleic acid molecules, which code a protein, which includes the amino acid sequence, which is coded by the insertion in plasmid DSM 15926;

- c) Nucleic acid molecules, which code a protein, the sequence of which has an identity of at least 70% with the amino acid sequence given under SEQ ID NO 4;
- d) Nucleic acid molecules, which code a protein, the sequence of which has an identity of at least 70% with the amino acid sequence, which is coded by the insertion in plasmid DSM 15926;
- e) Nucleic acid molecules, which include the nucleotide sequence shown under Seq ID NO 3 or a complimentary sequence;
- f) Nucleic acid molecules, which include the nucleotide sequence of the insertion contained in plasmid DSM 15926;
- g) Nucleic acid molecules, which have an identity of at least 70% with the nucleic acid sequences described under a), b), d) or e);
- h) Nucleic acid molecules, which hybridise with at least one strand of the nucleic acid molecules described under a), b), d), e) or f) under stringent conditions;
- i) Nucleic acid molecules, the nucleotide sequence of which deviates from the sequence of the nucleic acid molecules identified under a), b), e) or f) due to the degeneration of the genetic code; and
- j) Nucleic acid molecules, which represent fragments, allelic variants and/or derivatives of the nucleic acid molecules identified under a), b), c), d), e), f), g), h) or i).

The amino acid sequence shown in SEQ ID NO 4 codes a protein with the activity of a Class 3 branching enzyme from *Solanum tuberosum*.

- 25 The proteins coded from the different varieties of nucleic acid molecules according to the invention have certain common characteristics. These can include, for example, biological activity, molecular weight, immunological reactivity, conformation etc, as well as physical characteristics such as, for example, the running behaviour in gel electrophoresis, chromatographic behaviour, sedimentation coefficients, solubility, spectroscopic characteristics, stability; optimum pH, optimum temperature etc.

30 The molecular weight of the Class 3 branching enzyme from *Solanum tuberosum* derived from the amino acid sequence shown under SEQ ID NO 4 is ca. 103 kDa. The derived molecular weight of a protein according to the invention therefore

preferably lies in the range from 85 kDa to 120 kDa, preferably in the range from 95 kDa to 110 kDa and particularly preferably from ca. kDa 100 to 105 kDa.

- The present invention relates to nucleic acid molecules, which code a protein with the enzymatic activity of a Class 3 branching enzyme, wherein the coded protein has an identity of at least 70%, preferably of at least 80%, particularly preferably of at least 90% and especially preferably of 95% with the amino acid sequence specified under SEQ ID NO 4.
- 10 A plasmid containing a cDNA, which codes a Class 3 branching enzyme from *Solanum tuberosum*, was deposited with the Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH, Mascheroder Weg 1b, 38124 Braunschweig, Germany, in accordance with the Budapest Treaty on 15th September 2003 under the number DSM 15926. The amino acid sequence shown
- 15 SEQ ID NO 4 can be derived from the coding region of the cDNA sequence integrated in plasmid DSM 15926 and codes for a Class 3 branching enzyme from *Solanum tuberosum*. The present invention therefore also relates to nucleic acid molecules, which code a protein with the enzymatic activity of a Class 3 branching enzyme, which includes the amino acid sequence, which is coded by the insertion in
- 20 plasmid DSM 15926, wherein the coded protein has an identity of at least 70%, preferably of at least 80%, particularly preferably of at least 90% and especially preferably of 95% with the amino acid sequence, which can be derived from the insertion in DSM 15926.
- 25 The nucleic acid sequence shown SEQ ID NO 3 is a cDNA sequence, which includes the coding region for a Class 3 branching enzyme from *Solanum tuberosum*. The present invention therefore also relates to nucleic acid molecules, which code a Class 3 branching enzyme and the coding region of the nucleotide sequence shown under Seq ID NO 3 or a complimentary sequence, nucleic acid molecules, which
- 30 include the coding region of the nucleotide sequence of the insertion contained in plasmid DSM 15926 and nucleic acid molecules, which have an identity of at least 70%, preferably of at least 80%, particularly preferably of at least 90% and especially preferably of at least 95% with the said nucleic acid molecules.

With the help of the sequence information of the nucleic acid molecule according to the invention or with the help of the nucleic acid molecule according to the invention, it is now possible for the person skilled in the art to isolate homologous sequences from other plant species, preferably from starch-storing plants, preferably from plant species of the genus *Solanum*, particularly preferably from *Solanum tuberosum*. This can be carried out, for example, with the help of conventional methods such as the examination of cDNA or genomic banks with suitable hybridisation samples. The person skilled in the art knows that homologous sequences can also be isolated with the help of (degenerated) oligonucleotides and the use of PCR-based methods.

- 10 The examination of databases, such as are made available, for example, by EMBL (<http://www.ebi.ac.uk/Tools/index.htm>) or NCBI (National Center for Biotechnology Information, <http://www.ncbi.nlm.nih.gov/>), can also be used for identifying homologous sequences, which code for a Class 3 branching enzyme. In this case, one or more sequences are specified as a so-called query. This query sequence is
- 15 then compared by means of statistical computer programs with sequences, which are contained in the selected databases. Such database queries (e.g. blast or fasta searches) are known to the person skilled in the art and can be carried out by various providers.

If such a database query is carried out, e.g. at the NCBI (National Center for Biotechnology Information, <http://www.ncbi.nlm.nih.gov/>), then the standard settings, which are specified for the particular comparison inquiry, should be used. For protein sequence comparisons (blastp), these are the following settings: Limit entrez = not activated; Filter = low complexity activated; Expect value = 10; word size = 3; Matrix = BLOSUM62; Gap costs: Existence = 11, Extension = 1.

- 25 For nucleic acid sequence comparisons (blastn), the following parameters must be set: Limit entrez = not activated; Filter = low complexity activated; Expect value = 10; word size = 11.

With such a database search, the sequences described in the present invention can be used as a query sequence in order to identify further nucleic acid molecules and/or proteins, which code a Class 3 branching enzyme.

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With the help of the described methods, it is also possible to identify and/or isolate nucleic acid molecules according to the invention, which hybridise with the sequence specified under SEQ ID NO 3 and which code a Class 3 branching enzyme.

Within the framework of the present invention, the term "hybridising" means hybridisation under conventional hybridisation conditions, preferably under stringent conditions such as, for example, are described in Sambrook et al., Molecular Cloning, A Laboratory Manual, 2nd Ed. (1989) Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY). Particularly preferably, "hybridising" means hybridisation under the following conditions:

Hybridisation buffer:

2xSSC; 10xDenhardt solution (Ficoll 400+PEG+BSA; Ratio 1:1:1); 0.1% SDS; 5 mM EDTA; 50 mM Na₂HPO₄; 250 µg/ml herring sperm DNA; 50 µg/ml tRNA; or

10 25 M sodium phosphate buffer pH 7.2; 1 mM EDTA; 7% SDS

Hybridisation temperature: T=65 to 68°C

Wash buffer: 0.2xSSC; 0.1% SDS

Wash temperature: T=65 to 68°C.

In principle, nucleic acid molecules, which hybridise with the nucleic acid molecules according to the invention, can originate from any plant species, which expresses an appropriate protein, preferably they originate from starch-storing plants, preferably from species of the genus *Solanum*, particularly preferably from *Solanum tuberosum*. Nucleic acid molecules, which hybridise with the molecules according to the invention, can, for example, be isolated from genomic or from cDNA libraries. The identification and isolation of nuclear acid molecules of this type can be carried out using the nucleic acid molecules according to the invention or parts of these molecules or the reverse complements of these molecules, e.g. by means of hybridisation according to standard methods (see, for example, Sambrook et al., 1989, Molecular Cloning, A Laboratory Manual, 2nd Ed. Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY) or by amplification using PCR.

25 Nucleic acid molecules, which exactly or essentially have the nucleotide sequence specified under SEQ.ID NO 3 or parts of this sequence, can be used as hybridisation samples. The fragments used as hybridisation samples can also be synthetic fragments or oligonucleotides, which have been manufactured using established
30 synthesising techniques and the sequence of which corresponds essentially with that of a nucleic acid molecule according to the invention. If genes have been identified and isolated, which hybridise with the nucleic acid sequences according to the invention, then a determination of this sequence and an analysis of the

characteristics of the proteins coded by this sequence should be carried out in order to establish whether a Class 3 branching enzyme is involved. Homology comparisons on the level of the nucleic acid or amino acid sequence and a determination of the enzymatic activity are particularly suitable for this purpose. As described above, the activity of a Class 3 branching enzyme can take place by expression in *E. coli* strains, which themselves do not express an active branching enzyme (Kiel et al., 1987 Mol. Gen. Genet 207: 294-301); Guan et al., 1995, Proc. Natl. Acad. Sci. 92, 964-967).

The molecules hybridising with the nucleic acid molecules according to the invention particularly include fragments, derivatives and allelic variants of the nucleic acid molecules according to the invention, which code a Class 3 branching enzyme from plants, preferably from starch-storing plants, preferably from plant species of the genus *Solanum*, particularly preferably from *Solanum tuberosum*. In conjunction with the present invention, the term "derivative" means that the sequences of these molecules differ at one or more positions from the sequences of the nucleic acid molecules described above and have a high degree of identity with these sequences. Here, the deviation from the nucleic acid molecules described above can have come about, for example, due to deletion, addition, substitution, insertion or recombination.

Furthermore, identity means that functional and/or structural equivalence exists between the nucleic acid molecules concerned or the proteins coded by them. The nucleic acid molecules, which are homologous to the molecules described above and constitute derivatives of these molecules, are generally variations of these molecules, which constitute modifications, which execute the same biological function. At the same time, the variations can occur naturally, for example they can be sequences from other plant species, or they can be mutations, wherein these mutations may have occurred in a natural manner or have been introduced by objective mutagenesis. The variations can also be synthetically manufactured sequences. The allelic variants can be both naturally occurring variants and also synthetically manufactured variants or variants produced by recombinant DNA techniques. Nucleic acid molecules, which deviate from nucleic acid molecules according to the invention due to degeneration of the genetic code, constitute a special form of derivatives.

The proteins coded from the different derivatives of nucleic acid molecules according to the invention have certain common characteristics. These can include, for example, biological activity, substrate specificity, molecular weight, immunological reactivity, conformation etc, as well as physical characteristics such as, for example, the running behaviour in gel electrophoresis, chromatographic behaviour, sedimentation coefficients, solubility, spectroscopic characteristics, stability; optimum pH, optimum temperature etc.

The nucleic acid molecules according to the invention can be any nucleic acid molecules, in particular DNA or RNA molecules, for example cDNA, genomic DNA, mRNA etc. They can be naturally occurring molecules or molecules manufactured by genetic or chemical synthesis methods. They can be single-stranded molecules, which either contain the coding or the non-coding strand, or double-stranded molecules.

Furthermore, the present invention relates to nucleic acid molecules of at least 21, preferably more than 50 and particularly preferably more than 200 nucleotides length, which specifically hybridise with at least one nucleic acid molecule according to the invention. Here, specifically hybridise means that these molecules hybridise with nucleic acid molecules, which code a protein according to the invention, but not with nucleic acid molecules, which code other proteins. In particular, the invention relates to such nucleic acid molecules, which hybridise with transcripts of nucleic acid molecules according to the invention and, as a result, can hinder their translation. Such nucleic acid molecules, which specifically hybridise with the nucleic acid molecules according to the invention, can, for example, be constituents of antisense, RNAi or cosuppression constructs or ribozymes, or can be used as primers for PCR amplification.

In conjunction with the present invention, the term "identity" means a sequence identity over the whole length of the coding region of at least 60%, in particular an identity of at least 70%, preferably greater than 80%, particularly preferably greater than 90% and especially of at least 95%. In conjunction with the present invention, the term "identity" is to be understood to mean the number of amino

acids/nucleotides (identity) corresponding with other proteins/nucleic acids, expressed as a percentage. Identity is preferably determined by comparing the Seq. ID NO 4 or SEQ ID NO 3 with other proteins/nucleic acids with the help of computer programs. If sequences that are compared with one another have different lengths, the identity is to be determined in such a way that the number of amino acids, which have the shorter sequence in common with the longer sequence, determines the percentage quotient of the identity. Preferably, identity is determined by means of the computer program ClustalW, which is well known and available to the public (Thompson et al., Nucleic Acids Research 22 (1994), 4673-4680). ClustalW is made publicly available by Julie Thompson (Thompson@EMBL-Heidelberg.DE) and Toby Gibson (Gibson@EMBL-Heidelberg.DE), European Molecular Biology Laboratory, Meyerhofstrasse 1, D 69117 Heidelberg, Germany. ClustalW can also be downloaded from different Internet sites, including the IGBMC (Institut de Génétique et de Biologie Moléculaire et Cellulaire, B.P.163, 67404 Illkirch Cedex, France; <ftp://ftp-igbmc.u-strasbg.fr/pub/>) and the EBI (<ftp://ftp.ebi.ac.uk/pub/software/>) as well as from all mirrored Internet sites of the EBI (European Bioinformatics Institute, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SD, UK).

Preferably, Version 1.8 of the ClustalW computer program is used to determine the identity between proteins according to the invention and other proteins. In doing so, the following parameters must be set: KTUPLE=1, TOPDIAG=5, WINDOW=5, PAIRGAP=3, GAOPEN=10, GAPEXTEND=0.05, GAPDIST=8, MAXDIV=40, MATRIX=GONNET, ENDGAPS(OFF), NOPGAP, NOHGAP.

Preferably, Version 1.8 of the ClustalW computer program is used to determine the identity between the nucleotide sequence of the nucleic acid molecules according to the invention, for example, and the nucleotide sequence of other nucleic acid molecules. In doing so, the following parameters must be set:

KTUPLE=2, TOPDIAGS=4, PAIRGAP=5, DNAMATRIX:IUB, GAOPEN=10, GAPEXT=5, MAXDIV=40, TRANSITIONS: unweighted.

Basically, nucleic acid molecules according to the invention, can originate from any plant, preferably they originate from starch-storing plants, preferably from plant species of the genus *Solanum*, particularly preferably from *Solanum tuberosum*.

Furthermore, the invention relates to vectors, in particular plasmids, cosmids, viruses, bacteriophages and other common vectors in genetic engineering, which contain the nucleic acid molecules according to the invention described above.

- 5 In a preferred embodiment, the nucleic acid molecules according to the invention contained in the vectors are linked with regulatory sequences, which guarantee expression in prokaryotic or eukaryotic cells. Here, the term "expression" can mean both transcription as well as transcription and translation. In this case, the nucleic acid molecules according to the invention can be present in "sense"
10 orientation and/or in "antisense" orientation to the regulatory sequences.

- Regulatory sequences for expression in prokaryotic organisms, e.g. *E. coli*, and in eukaryotic organisms are adequately described in the literature, in particular those for expression in yeast such as *Saccharomyces cerevisiae*, for example. An overview
15 of different expression systems for proteins in different host organisms can be found, for example, in Methods in Enzymology 153 (1987), 383-516 and in Bitter et al. (Methods in Enzymology 153 (1987), 516-544).

- For expressing the nucleic acid molecules, which code a Class 3 branching enzyme,
20 in sense and/or antisense orientation in vegetable cells, these are preferably linked with regulatory DNA sequences, which guarantee transcription in vegetable cells. In particular, these include promoters. In general, any promoter that is active in vegetable cells is eligible for expression.

- At the same time, the promoter can be chosen so that expression takes place
25 constitutively or only in a certain tissue, at a certain stage of the plant development or at a time determined by external influences. The promoter can be homologous or heterologous both with respect to the plant and with respect to the nucleic acid molecule.

- Suitable promoters are, for example, the promoter of the 35S RNA of the cauliflower
30 mosaic virus and the ubiquitin promoter from maize for constitutive expression, the patatin promoter B33 (Rocha-Sosa et al., EMBO J. 8 (1989), 23-29) for tuber-specific expression in potatoes or a promoter, which only ensures expression in photosynthetically active tissues, e.g. the ST-LS1 promoter (Stockhaus et al., Proc.

Natl. Acad. Sci. USA 84 (1987), 7943-7947; Stockhaus et al., EMBO J. 8 (1989), 2445-2451) or, for endosperm-specific expression of the HMG promoter from wheat, the USP promoter, the phaseolin promoter, promoters of zein genes from maize (Pedersen et al., Cell 29 (1982), 1015-1026; Quatroccio et al., Plant Mol. Biol. 15
5 (1990), 81-93), glutelin promoter (Leisy et al., Plant Mol. Biol. 14 (1990), 41-50; Zheng et al., Plant J. 4 (1993), 357-366; Yoshihara et al., FEBS Lett. 383 (1996), 213-218) or shrunken-1 promoter (Werr et al., EMBO J. 4 (1985), 1373-1380). However, promoters can also be used, which are only activated at a time determined by external influences (see for example WO 9307279). Promoters of heat-shock
10 proteins, which allow simple induction, can be of particular interest here. Furthermore, seed-specific promoters can be used, such as the USP promoter from *Vicia faba*, which guarantees seed-specific expression in *Vicia faba* and other plants (Fiedler et al., Plant Mol. Biol. 22 (1993), 669-679; Bäumlein et al., Mol. Gen. Genet. 225 (1991), 459-467).

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Furthermore, a termination sequence (polyadenylation signal) can be present, which is used for adding a poly-A tail to the transcript. A function in the stabilisation of the transcripts is ascribed to the poly-A tail. Elements of this type are described in the literature (cf. Gielen et al., EMBO J. 8 (1989), 23-29) and can be exchanged at will.

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In a further embodiment, the present invention relates to vectors, which contain DNA molecules, which code at least one antisense RNA, which effects a reduction in the expression of at least one endogenous gene, which codes a Class 3 branching enzyme.

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In a further special embodiment, the present invention relates to vectors, which contain DNA molecules, which by means of a cosuppression effect lead to a reduction in the expression of at least one endogenous gene, which codes a Class 3 branching enzyme.

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In a further embodiment, the present invention relates to vectors, which contain DNA molecules, which code at least one ribozyme, which splits specific transcripts of at least one endogenous gene, which codes a Class 3 branching enzyme.

In a further embodiment, the present invention relates to vectors, which contain DNA molecules, which simultaneously code at least one antisense RNA and at least one sense RNA, wherein the said antisense RNA and the said sense RNA form a double-stranded RNA molecule, which effects a reduction in the expression of at least one endogenous gene, which codes a Class 3 branching enzyme (RNAi technology).

A further subject of the present invention is a host cell, in particular a prokaryotic or eukaryotic cell, which is genetically modified with a nucleic acid molecule according to the invention and/or with a vector according to the invention, as well as cells, which originate from host cells of this type and which contain the genetic modification according to the invention.

In a preferred embodiment, the invention relates to host cells, in particular prokaryotic or eukaryotic cells, which have been transformed using the nucleic acid molecule according to the invention or a vector according to the invention, as well as host cells, which originate from host cells of this type and which contain the described nucleic acid molecules or vectors according to the invention.

The host cells can be bacteria (e.g. *E. coli*) or fungus cells (e.g. yeast, in particular *S. cerevisiae*, *Agaricus*, in particular *Agaricus bisporus*), as well as vegetable or animal cells. Here, the term "transforms" means that the cells according to the invention are genetically modified with a nucleic acid molecule according to the invention inasmuch as they contain at least one nucleic acid molecule according to the invention in addition to their natural genome. This can be freely present in the cell, possibly as a self-replicating molecule, or it can be stably integrated in the genome of the host cell.

The host cells are preferably microorganisms. Within the framework of the present application, these are understood to mean all bacteria and all protista (e.g. fungi, in particular yeast and algae), as defined, for example, in Schlegel "Allgemeine Mikrobiologie" (Georg Thieme Verlag (1985), 1-2).

It is especially preferred if the host cells according to the invention are plant cells. In principle, these can be plant cells from any plant species, i.e. both monocotyledonous and dicotyledonous plants. Preferably, these will be plant cells

from useful agricultural plants, i.e. from plants, which are cultivated by people for the purposes of food or for technical, in particular industrial purposes. The invention relates preferably to plant cells and plants from starch-storing plants (maize, rice, wheat, rye, oat, barley, cassava, potato, sago, mung bean, pea or sorghum); in particular, plant cells from maize, rice, wheat or potato plants are particularly preferred.

A further subject of the present invention are proteins with the enzymatic activity of a Class 3 branching enzyme, chosen from the group consisting of

- 10 a) Proteins, which include the amino acid sequence specified under SEQ ID NO 4;
- b) Proteins, which are coded by the coding region of the DNA inserted in the plasmid DSM 15926; or
- 15 c) Proteins, which have an identity of at least 70% with the amino acid sequence of the proteins identified under a) or b).

In a further embodiment, the present invention relates to proteins with the enzymatic activity of a Class 3 branching enzyme, wherein the coded protein has an identity of at least 70%, preferably of at least 80%, particularly preferably of at least 90% and especially preferably of 95% with the amino acid sequence specified under SEQ ID NO 4 or with the amino acid sequence of a Class 3 branching enzyme coded by the insertion in plasmid DSM 15926.

In a further embodiment, the invention also relates to proteins, which are coded by nucleic acid molecules according to the invention.

In a preferred embodiment, the present invention relates to a protein with the enzymatic activity of a Class 3 branching enzyme, wherein the Class 3 branching enzyme originates from a potato plant.

Surprisingly, it has been found that plant cells and plants, which have a reduced activity of a Class 3 branching enzyme, synthesise a starch, which is modified in comparison with starch from wild type plant cells or wild type plants.

In conjunction with the present invention, the term "modified starch" means that the starch has changed physical-chemical characteristics compared with non-modified starch obtainable from corresponding wild type plant cells or wild type plants that
5 have not been genetically modified.

In a preferred embodiment of the present invention, the modified starch is native starch.

In conjunction with the present invention, the term "native starch" means that the
10 starch is isolated from plants according to the invention, harvestable plant plants according to the invention or propagation material of plants according to the invention by methods known to the person skilled in the art.

Starch is a classical additive for many foodstuffs in which it essentially takes over the
15 function of binding aqueous additives or increasing the viscosity, or brings about an increased formation of gel. Important characteristic features are the flow and sorption behaviour, the source and sticking temperature, the viscosity and thickening performance, the solubility of the starch, the transparency and paste structure, the heat, shearing and acidic stability, the tendency to retrogradation, the ability to form a
20 film, the freezing/thawing stability, the digestibility as well as the ability to form complexes with, for example, inorganic or organic ions.

In the area of the non-foodstuffs industry, starch can be used, for example, as an auxiliary substance for different manufacturing processes or as an additive in technical products. Particular mention must be made here of the paper and
25 cardboard industry where starch is used as an auxiliary substance. Here, the starch is primarily used for retardation (holding back of solids), the bonding of filler and fine material particles, as a consolidation material and for dehydration. In addition to this, the favourable characteristics of starch with regard to stiffness, hardness, sound, grip, shine, smoothness and resistance to splitting as well as the surfaces are also
30 fully utilised.

A further major area of use of starches is in the adhesive industry, where the possible applications are divided into four sub-areas. Use as a pure starch adhesive, use with starch adhesives prepared with special chemicals, use of starch as an additive to

synthetic resins and polymer dispersions, and the use of starches as a stretching medium for synthetic adhesives.

Furthermore, starches can be used as additives for building materials (e.g. plasterboard sheets, ready-mixed concrete, plaster and mineral fibres), for the manufacture of media for stabilising soil, as a functional aid in plant protection media or fertilisers, as a functional aid in the pharmaceutical industry (e.g. as a bonding medium, tablet dispersal medium, in lubricating and vulnerary powders) and the cosmetic industry (as a carrier of additives), as a strengthening additive for coal and briquettes, as a flocculation medium (e.g. in the preparation of carbon sludge) and as a bonding medium, e.g. in Betonit.

Plant cells according to the invention and plants according to the invention synthesise a modified starch in comparison with starch of corresponding wild type plant cells or wild type plants that have not been genetically modified. In its physical-chemical characteristics, e.g. the amylopectin/amylose ratio, the degree of branching, the phosphate content, the average chain length, the viscosity behaviour, the starch grain size, the side chain distribution and/or the starch grain form, the modified starch is changed in comparison with the synthesised starch in wild type plant cells or plants so that it is better suited for use in particular application areas, for example.

The present invention therefore also relates to modified starches obtainable or isolated from plant cells according to the invention or plants according to the invention, from propagation material according to the invention or from harvestable plant parts according to the invention.

In a particularly preferred embodiment, the present invention relates to modified potato starch.

Furthermore the present invention relates to a method for the manufacture of a modified starch including the step of extracting the starch from a plant cell according to the invention or from a plant according to the invention, from propagation material according to the invention of such a plant and/or from harvestable plant parts according to the invention of such a plant, preferably from starch-storing parts

according to the invention of a plant. Preferably, such a method also includes the step of harvesting the cultivated plants or plant parts and/or the propagation material of these plants before the extraction of the starch and, further, particularly preferably the step of cultivating plants according to the invention before harvesting.

5

Methods for extracting starches from plants or from starch-storing parts of plants are known to the person skilled in the art. Furthermore, methods for extracting starch from different starch-storing plants are described, e.g. in Starch: Chemistry and Technology (Publisher: Whistler, BeMiller and Paschall (1994), 2nd Edition, Academic Press Inc. London Ltd; ISBN 0-12-746270-8; see e.g. Chapter XII, Page 412-468: Maize and Sorghum Starches: Manufacture; by Watson; Chapter XIII, Page 469-479: Tapioca, Arrowroot and Sago Starches: Manufacture; by Corbishley and Miller; Chapter XIV, Page 479-490: Potato starch: Manufacture and Uses; by Mitch; Chapter XV, Page 491 to 506: Wheat starch: Manufacture, Modification and Uses; by Knight and Oson; and Chapter XVI, Page 507 to 528: Rice starch: Manufacture and Uses; by Rohmer and Klem; Maize starch: Eckhoff et al., Cereal Chem. 73 (1996), 54-57, the extraction of maize starch on an industrial scale is generally achieved by so-called "wet milling"). Devices, which are in common use in methods for extracting starch from plant material are separators, decanters, hydrocyclones, spray dryers and fluid bed dryers.

In conjunction with the present invention, the term "starch-storing parts" is to be understood to mean such parts of a plant in which, in contrast to transitory leaf starch, starch is stored as a deposit for surviving for longer periods. Preferred starch-storing parts are tubers, storage roots, seeds or endosperm; particularly preferred are potato tubers or the endosperm of maize, wheat or rice plants.

Modified starch obtainable by the method according to the invention is also the subject matter of the present invention.

30

Furthermore, the use of plant cells according to the invention or plants according to the invention for manufacturing a modified starch are the subject matter of the present invention.

The person skilled in the art knows that the characteristics of starch can be changed by thermal, chemical, enzymatic or mechanical derivation, for example. Derived starches are particularly suitable for different applications in the foodstuffs and/or non-foodstuffs sector. The starches according to the invention are better suited as a starting substance for the manufacture of derived starches than conventional starches. In the manufacture of derived starch, they are distinguished by better processing capability and lead to new products, as a modified starch is used as a new starting material for the derivation process.

10

The present invention therefore also relates to the manufacture of a derived starch, wherein modified starch according to the invention is derived retrospectively.

In conjunction with the present invention, the term "derived starch" is to be understood to mean a modified starch according to the invention, the characteristics of which have been retrospectively changed after isolation from vegetable cells with the help of chemical, enzymatic, thermal or mechanical methods.

In a preferred embodiment of the present invention, the derived starch according to the invention is starch that has been heat-treated and/or acid-treated.

20 In a further preferred embodiment, the derived starches are starch ethers, in particular starch alkyl ethers, O-allyl ethers, hydroxylalkyl ethers, O-carboxylmethyl ethers, nitrogen-containing starch ethers, phosphate-containing starch ethers or sulphur-containing starch ethers.

25 In a further preferred embodiment, the derived starches are cross-linked starches.

In a further preferred embodiment, the derived starches are starch graft polymers.

In a further preferred embodiment, the derived starches are oxidised starches.

30

In a further preferred embodiment, the derived starches are starch esters, in particular starch esters, which have been introduced into the starch using organic

acids. Particularly preferably these are phosphate, nitrate, sulphate, xanthate, acetate or citrate starches.

The derived starches according to the invention are suitable for different applications
5 in the foodstuffs and/or non-foodstuffs sector. Methods for manufacturing derived starches according to the invention are known to the person skilled in the art and are adequately described in the general literature. An overview on the manufacture of derived starches can be found, for example, in Orthoefer (in Corn, Chemistry and Technology, 1987, eds. Watson und Ramstad, Chapter 16, 479-499).

10

Derived starch obtainable by the method according to the invention for manufacturing a derived starch is also the subject matter of the present invention.

Furthermore, the use of modified starches according to the invention for
15 manufacturing derived starch is the subject matter of the present invention.

Description of sequences

SEQ ID NO 1: Nucleic acid sequence containing the coding region of the 3'-
20 area of a Class 3 branching enzyme from *Solanum tuberosum* (cv Désirée). This sequence is inserted in plasmid AN 46-196.

SEQ ID NO 2: Nucleic acid sequence containing the coding region of the 5'-
area of a Class 3 branching enzyme from *Solanum tuberosum* (cv Désirée). This
25 sequence is inserted in plasmid AN 47-196.

SEQ ID NO 3: Nucleic acid sequence containing the full coding region of a
Class 3 branching enzyme from *Solanum tuberosum* (cv Désirée). This sequence is
inserted in plasmid AN 49 and was deposited with the Deutsche Sammlung von
30 Mikroorganismen und Zellkulturen GmbH, Mascheroder Weg 1b, 38124
Braunschweig, Germany, in accordance with the Budapest Treaty on 15th
September 2003 under the number DSM 15926.

SEQ ID NO 4: Amino acid sequence coding a Class 3 branching enzyme from *Solanum tuberosum* (cv Désirée). This sequence can be derived from the nucleic acid sequence inserted in plasmid AN 49 or from the nucleic acid sequence described under SEQ ID NO 3.

5

SEQ ID NO 5: Nucleic acid sequence containing the full coding region of a Class 3 branching enzyme from *Solanum tuberosum* (cv Désirée). This sequence has been obtained by combining the nucleic acid sequences described under SEQ ID NO 1 and SEQ ID NO 2. This nucleic acid sequence constitutes an allelic variant of the nucleic acid sequence described under SEQ ID NO 3 coding a Class 3 branching enzyme.

SEQ ID NO 6: Amino acid sequence coding a Class 3 branching enzyme from *Solanum tuberosum* (cv Désirée). This sequence can be derived from the nucleic acid sequence described under SEQ ID NO 5 and constitutes an allelic variant of the amino acid sequence described under SEQ ID NO 4 coding a Class 3 branching enzyme.

General methods

20 The following methods were used in the examples:

Demonstration of the activity of a Class 3 branching enzyme

The activity of a Class 3 branching enzyme was demonstrated with the help of non-denaturing gel electrophoresis as follows:

25 To isolate proteins from plants, the test material was ground with a pestle in liquid nitrogen, absorbed into an extraction buffer (50 mM Na citrate, pH 6.5; 1 mM EDTA, 4 mM DTT) and, after centrifugation (10 min, 14.000 g, 4 °C), was used directly for measurement of the protein content according to Bradford. Subsequently, 5µg to 20 µg total protein extract was mixed with 4X loading buffer (20% glycerol, 125 mM Tris HCl, pH 6.8) and loaded onto a BE activity gel. The BE activity gel was made up as follows: 2.5 ml 30% acrylamide:0.8% bisacrylamide, 0.1 ml running buffer, 7.4 ml H₂O, 10% ammonium persulphate solution and 5 µl N,N,N',N'-

30

tetramethylethylenediamine (TEMED). The running buffer (RB) was made up as follows: RB = 30.2 g Tris base, pH 8.0, 144 g glycine on 1 L H₂O. On completion of the gel run, each of the gels was incubated overnight at 37 °C in 25 ml "phosphorylase buffer" (25 ml 1M Na citrate pH 7.0, 0.47 g glucose-1-phosphate, 5 12.5 mg AMP, 2.5 mg phosphorylase a/b from "rabbit"). The gels were coloured with Lugol's solution.

Starch analysis

a) Determination of the amylose content and of the amylose/amylopectin ratio

10 Starch was isolated from potato plants by standard methods, and the amylose content and the amylose:amylopectin ratio was determined by the method described by Hovenkamp-Hermelink et al. (Potato Research 31, (1988), 241-246).

b) Determination of the phosphate content

15 In starch, the positions C2, C3 and C6 of the glucose units can be phosphorylated. To determine the C6-P content of starch, 50 mg of starch are hydrolysed for 4 h at 95°C in 500 µl of 0.7 M HCl. The samples are then centrifuged for 10 minutes at 15500xg and the supernatants are removed. 7 µl of the supernatants are mixed with 193 µl of imidazole buffer (100 mM imidazole, pH 7.4; 5 mM MgCl₂, 1 mM EDTA and 20 0.4 mM NAD). The measurement was carried out in a photometer at 340 nm. After the base absorption had been established, the enzyme reaction was started by addition of 2 units glucose-6-phosphate dehydrogenase (from *Leuconostoc mesenteroides*, Boehringer Mannheim). The change in absorption is directly proportional to the concentration of the G-6-P content of the starch.

25

The total phosphate content was determined by the method of Ames (Methods in Enzymology VIII, (1966), 115-118).

Approximately 50 mg of starch are treated with 30 µl of ethanolic magnesium nitrate solution and ashed for 3 hours at 500°C in a muffle oven. The residue is treated with 30 300 µl of 0.5 M hydrochloric acid and incubated for 30 minutes at 60°C. One aliquot is subsequently made up to 300 µl 0.5 M hydrochloric acid and this is added to a

mixture of 100 µl of 10% ascorbic acid and 600 µl of 0.42% ammonium molybdate in 2 M sulphuric acid and incubated for 20 minutes at 45°C.

This is followed by a photometric determination at 820 nm with a phosphate calibration series as standard.

5

c) Determination of the viscosity characteristics by means of a Rapid Visco Analyser (RVA)

2 g of starch (DM) are taken up in 25 ml of H₂O (VE-type water, conductivity of at least 15 mega ohm) and used for the analysis in a Rapid Visco Analyser Super3 (Newport Scientific Pty Ltd., Investmet Support Group, Warriewood NSW 2102, Australia). The apparatus is operated following the manufacturer's instructions. The viscosity values are indicated in Centipoise (cP) in accordance with the manufacturer's operating manual, which is incorporated into the description herewith by reference. To determine the viscosity of the aqueous starch solution, the starch suspension is first stirred for 10 seconds at 960 rpm and subsequently heated at 50°C at a stirring speed of 160 rpm, initially for a minute (step 1). The temperature was then raised from 50°C to 95°C at a heating rate of 12°C per minute (step 2). The temperature is held for 2.5 minutes at 95°C (step 3) and then cooled from 95°C to 50°C at 12°C per minute (step 4). In the last step (step 5), the temperature of 50°C is held for 2 minutes. The viscosity is determined during the entire duration.

After the programme has ended, the stirrer is removed and the beaker covered. The gelatinized starch is now available for the texture analysis after 24 hours incubation at room temperature.

25

The profile of the RVA analysis contains parameters which are shown for the comparison of different measurements and substances. In the context of the present invention, the following terms are to be understood as follows:

1. Maximum viscosity (RVA Max)

30 The maximum viscosity is understood as meaning the highest viscosity value, measured in cP, obtained in step 2 or 3 of the temperature profile.

2. Minimum viscosity (RVA Min)

The minimum viscosity is understood as meaning the lowest viscosity value, measured in cP, observed in the temperature profile after the maximum viscosity. Normally, this takes place in step 3 of the temperature profile.

3. Final viscosity (RVA Fin)

- 5 The final viscosity is understood as meaning the viscosity value, measured in cP, observed at the end of the measurement.

4. Setback (RVA Set)

- What is known as the "setback" is calculated by subtracting the value of the final viscosity from that of the minimum occurring after the maximum viscosity in the curve.

5. Gelatinization temperature (RVA PT)

The gelatinization temperature is understood as meaning the point in time of the temperature profile where, for the first time, the viscosity increases drastically for a brief period.

15 d) Determination of the gel strength (Texture Analyser)

- 2 g of starch (DM) are gelatinized in the RVA apparatus in 25 ml of an aqueous suspension (temperature programme: see item d) "Determination of the viscosity characteristics by means of a Rapid Visco Analyser (RVA)") and subsequently stored for 24 hours at room temperature in a sealed container. The samples are fixed under the probe (round piston with planar surface) of a Texture Analyser TA-XT2 from Stable Micro Systems (Surrey, UK) and the gel strength was determined using the following parameters:

- | | | | |
|----|---|----------------------|---------------------|
| | - | Test speed | 0.5 mm/s |
| 25 | - | Depth of penetration | 7 mm |
| | - | Contact surface | 113 mm ² |
| | - | Pressure | 2 g |

30 e) Analysis of the side-chain distribution of the amylopectin by means of ion-exchange chromatography

To separate amylose and amylopectin, 200 mg of starch are dissolved in 50 ml reaction vessels, using 12 ml of 90% (v/v) DMSO in H₂O. After addition of 3 volumes of ethanol, the precipitate is separated by centrifugation for 10 minutes at about

- 1800xg at room temperature (RT). The pellet is then washed with 30 ml of ethanol, dried and dissolved in 40 ml of 1% (w/v) NaCl solution at 75°C. After the solution has cooled to 30°C, approximately 90 mg of thymol are added slowly, and this solution is incubated for at least 60 h at 30°C. The solution is then centrifuged for 30 minutes at
- 5 2000xg (RT). The supernatant is then treated with 3 volumes of ethanol, and the amylopectin which settles out is separated by centrifugation for 5 minutes at 2000xg (RT). The pellet (amylopectin) is then washed with ethanol and dried using acetone. By addition of DMSO to the pellet, one obtains a 1% solution, of which 200 µl are treated with 345 µl of water, 10 µl of 0.5 M sodium acetate (pH 3.5) and 5 µl of
- 10 isoamylase (dilution 1:10; Megazyme) and incubated for about 16 hours at 37°C. A 1:5 aqueous dilution of this digest is subsequently filtered through a 0.2 µm filter, and 100 µl of the filtrate are analysed by ion chromatography (HPAEC-PAD, Dionex). Separation was performed using a PA-100 column (with suitable precolumn), while detection was performed amperometrically. The elution conditions were as follows:
- 15 Solution A - 0.15M NaOH
Solution B - 1 M sodium acetate in 0.15M NaOH

t (min)	Solution A (%)	Solution B (%)
5	0	100
35	30	70
45	32	68
60	100	0
70	100	0
72	0	100
80	0	100
Stop		

20 **Table 1:** Composition of the elution buffer for the side chain analysis of the amylopectin at different times during the HPAEC-PAD Dionex analysis. Between the times stated, the composition of the elution buffer changes in each case linearly.

The determination of the relative amount of short side chains in the total of all side chains is carried out via the determination of the percentage of a particular side chain

in the total of all side chains. The total of all side chains is determined via the determination of the total area under the peaks which represent the polymerization degrees of DP 6 to 34 in the HPCL chromatogram.

The percentage of a particular side chain in the total of all side chains is determined via the determination of the ratio of the area under the peak which represents this side chain in the HPLC chromatogram to the total area. The programme Chromelion 6.20 Version 6.20 from Dionex, USA, was used for determining the peak areas.

f) Determination of the activity of the BEIII protein

This was carried out as specified in the example.

g) DSC-analysis („Differential Scanning Calorimetry“)

Investigations with the aid of DSC-analysis have been done by the method described by WO 01/19975. 10 mg starch treated with 30 µl H₂O (VE-type water, conductivity of at least 15 mega ohm) were sealed in stainless steel pans (volume 50 µl). The pan is heated from 20°C to 150°C at a rate of 10°C per minute in a Diamond DSC-instrument (Perkin Elmer). The programme Pyres from Perkin Elmer was used for determining the data.

Examples

Example 1

Cloning of a full-length sequence coding a Class 3 branching enzyme from *Solanum tuberosum*

The gene sequence coding for this Class 3 branching enzyme in *Solanum tuberosum* has not previously been described.

By sequence comparisons with different branching enzymes, a domain was identified, with the help of which EST databases were examined. In doing so, the EST TC73137 (TIGR database; http://www.tigr.org/tigr-scripts/tgi/tc_report.pl?tc=TC73137&species=potato) from potato was identified.

With the help of the primers B1_Asp (GAT GGG TAC CAG CAC TTC TAC TTG GCA GAG G) and B2_Sal (TCA AGT CGA CCA CAA CCA GTC CAT TTC TGG), a sequence from a tuber-specific cDNA bank from *Solanum tuberosum* (cv. Désirée) corresponding to this EST sequence was amplified. Attempts to use leaf-specific, "sink"-tissue-specific or "source"-tissue-specific cDNA banks as a template for the PCR reaction led to no amplification.

In order to amplify the whole coding sequence of the branching enzyme concerned, which up to now had also included unknown sequences, primers were manufactured, which were complimentary to the ends of the previously known sequence and vector sequences of the cDNA banks concerned. With all the primer combinations for the amplification of a full-length sequence of a Class 3 branching enzyme used in this approach, it was not possible to amplify any further area. Hereupon, EST databases of tomato were examined again.

In this case, two ESTs from tomato were identified (TIGR database; BG127920 and TC130382), which either had a high homology to the amplification of the Class 3 branching enzyme from potato described above (TC130382) and (BG127920) respectively, or to the putative branching enzyme gene from arabidopsis (GenBank: GP|9294564|dbj|BAB02827.1).

Primers were now manufactured again in order to also amplify previously unknown sequences of the Class 3 branching enzyme. By means of PCR, the 3'-area of the Class 3 branching enzyme was amplified from a cDNA bank, made from tubers of *Solanum tuberosum* (cv. Désirée), with the primers KM2_Spe (5'-TCAAAGTAGTCACAACCAGTCCATTCTGG-3') and So_putE (5'-CACTTTAGAAGGTATCAGAGC-3'). The fragment with a size of ca. 1 kb that was obtained was cloned undirectedly in the pCR4-TOPO vector from Invitrogen (product number: 45-0030). The plasmid produced was designated as AN 46-196. The sequence of the inserted fragments in the plasmid AN 46-196 is shown under SEQ ID NO 1.

30

The 5'-area was likewise amplified by means of PCR technology and using the primers So_put5' (5'-GTATTTCTGCGAAGGAACGACC-3') and So_putA (5'-AACAAATGCTCTCTCTGTCGG-3') from the same cDNA bank. The fragment with a

size of ca. 2 kb that was obtained was cloned undirectedly in the pCR4-TOPO vector from Invitrogen (product number: 45-0030). The plasmid produced was designated as AN 47-196. The sequence of the inserted fragments in the plasmid AN 47-196 is shown under SEQ ID NO 2.

5

Primers were now manufactured again in order to amplify a full-length sequence.

The following primers were used: SO_putA (AACAATGCTCTCTGTCTCGG) and SO_putE (CACTTTAGAAGGTATCAGAGC). A PCR product with an approximate size of 3.2 kb was obtained and was cloned in the pCR2.1 vector from Invitrogen

10 (product number: 45-0030). The plasmid obtained (filed under DSM 15926) was designated as AN 49. The sequence of the inserted fragments in the plasmid AN 49 is shown under SEQ ID NO 3.

Example 2

15 Information on vectors and plasmids

Information on vector AN 54-196

AN 54-196 is a derivative of the plasmid pBinB33-Hyg, to which was added a part sequence of the Class 3 branching enzyme gene as an "inverted repeat, (RNAi technology) under the control of the promoters of the patatin gene B33 from *Solanum*

20 *tuberosum* (Rocha-Sosa et al., 1989). For this purpose, first of all, a PCR product with the primers B1_Asp (GAT GGG TAC CAG CAC TTC TAC TTG GCA GAG G) and B2_Sal (TCA AGT CGA CCA CAA CCA GTC CAT TTC TGG) from a tuber-specific cDNA bank from *Solanum tuberosum* (cv. Désirée) was amplified, as a result of which the sites Asp718 and SalI were added. The PCR product obtained (625 bp)

25 was cloned in "antisense" orientation to the B33 promoter via these two sites. A second PCR fragment, which was amplified with the primers B3_Sal (GCT TGT CGA CGG GAG AAT TTT GTC CAG AGG) and B4_Sal (GAT CGT CGA CAG CAC TTC TAC TTG GCA GAG G) from a tuber-specific cDNA bank from *Solanum tuberosum* (cv. Désirée) and which is identical to the 301 bp of the first fragment, was cloned via

the Sall site behind the first fragment, but in "sense" orientation to the B33 promoter. This arrangement is described as "inverted repeat" (RNAi technology).

Information on vector pBinB33-Hyg

- 5 Starting from the plasmid pBinB33, the *EcoRI-HindIII* fragment including the B33 promoter, a part of the polylinker, and the ocs terminator were cut out and spliced into the correspondingly cut vector pBIB-Hyg (Becker, 1990).

The plasmid pBinB33 was obtained by splicing the promoter of the patatin gene B33 from *Solanum tuberosum* (Rocha-Sosa et al., 1989) as a *DraI* fragment (nucleotide –
10 1512 - +14) into the vector pUC19 cut with *SstI*, the ends of which had been smoothed with the help of the T4 DNA polymerase. This resulted in the plasmid pUC19-B33. The B33 promoter was cut out from this plasmid with *EcoRI* and *SmaI* and spliced into the correspondingly cut vector pBinAR. This resulted in the vegetable expression vector pBinB33.

- 15 The plasmid pBinAR is a derivative of the vector plasmid pBin19 (Bevan, 1984) and was constructed as follows:

A fragment of length 529 Bp, which included the nucleotides 6909-7437 of the 35S RNA promoter of the cauliflower mosaic virus (Pietrzak et al., 1986, Nucleic Acids Research 14, 5857-5868), was isolated as an *EcoRI/KpnI* fragment from the plasmid
20 pDH51 (Pietrzak et al., 1986) and spliced between the *EcoRI* and *KpnI* sites of the polylinker from pUC18. This resulted in the plasmid pUC18-35S.

With the help of the restriction endonucleases *HindIII* und *PvuII*, a fragment of length 192 Bp, which included the polyadenylation signal (3'-end) of the octopin synthase gene (gene 3) of the T-DNA of the Ti plasmid pTiACH5 (Gielen et al., 1984)
25 (nucleotides 11749-11939) was isolated from the plasmid pAGV40 (Herrera-Estrella et al., 1983). After the addition of *SspI* linkers to the *PvuII* site, the fragment was spliced between the *SphI* and *HindIII* site from pUC18-35S. This resulted in the plasmid pA7.

The whole polylinker containing the 35S promoter and the ocs terminator with *EcoRI*
30 and *HindIII* was cut out of pA7 and spliced into the correspondingly cut pBin19. This resulted in the vegetable expression vector pBinAR (Höfgen and Willmitzer, 1990).

Example 3

Genetically modified plants with reduced Class 3 branching enzyme activity

- 5 In order to produce transgenic potato plants, which have a reduced expression of a Class 3 branching enzyme gene, the T-DNA of the plasmid AN 54-196 was transferred into potato plants of the variety Désirée with the help of agrobacteria, as described in Rocha-Sosa et al. (EMBO J. 8, (1989), 23-29). The plants of the variety Désirée obtained by transformation with the plasmid AN 53-196 were designated as
- 10 369SO.

- Analysis with the help of non-denaturising gel electrophoresis of protein extracts from tubers of wild type plant cells and/or protein extracts from genetically modified plants (396SO), showed that the genetically modified plant cells have a reduced activity of a Class 3 branching enzyme in comparison with protein extracts from tubers of wild
- 15 type plant cells.

- Additionally mRNA of tuber material was extracted with standard methods and applied to quantitative RT-PCR analysis. The analysis were performed with a PCR-instrument ABI Prism 7700 from Applied Biosystems using the primer St_BE-r2 (5'-TCA GGT CTA CAA GTT GAC CCG A-3'), St_BE-r2 (5'-GTA GAA CCT TCC CTT
- 20 TTG TGT GA-3') and St_BE-Fam (5'-Fam-CAT GAT CAC TCT AGC AAT CAA AGT GCC-Tamra-3'). It could be shown that given plants showed reduced transcript in comparison with the corresponding wild type.

Example 4

25 Potato starch extraction process

All tubers of one line (0,3 to 0,7 kg) are processed jointly in a commercially available juice extractor (Multipress automatic MP80, Braun). The starch-containing fruit water is collected in a 1-l bucket (ratio bucket height: bucket diameter = approx. 1.1) containing 20 ml of tap water together with a spoon-tipful (approx. 0,3-0,4 g) of

sodium disulphite. The bucket is subsequently filled completely with tap water. After the starch has been allowed to settle for 2 hours (h), the supernatant is decanted off, the starch is resuspended in 1 l of tap water and poured over a sieve with a mesh size of 125 µm. After 2 h (starch has again settled at the bottom of the bucket), the aqueous supernatant is again decanted off. This wash step is repeated 3 more times so that the starch is resuspended a total of 5 times in fresh tap water. Thereafter, the starches are dried at 37°C to a water content of 12-17% and homogenized using a pestle and mortar. The starches are now available for analyses.

10 **Example 5**

Analysis of the starch from plants with reduced BEIII gene expression

The starch from various independent lines of plants named 369SO were isolated from potato tubers. The physico-chemical properties of this starch were subsequently analysed. The results of the characterization of the modified starches are shown in the following for an example of a selection of certain plant lines. The analyses were carried out by the methods described hereinabove.

a) RVA Analysis

	RVA Max (%)	RVA Min (%)	RVA Fin (%)	RVA Set (%)	RVA PT (%)	Gel strength
cv.Desiree	100	100	100	100	100	100
369SO048	91	64	90	N.d.	98	128
369SO050	84	84	89	112	98	127
369SO052	94	85	88	101	98	N.d.
369SO106	91	87	89	99	98	N.d.
369SO129	87	88	93	114	99	138

20 **Table 2:** Parameters of the RVA analysis of starch isolated from wild-type plants (cv. Desiree), plants with a reduced activity of a BEIII protein (369SO) in per cent based on data of starch of the wild type. The RVA analysis was carried out as described in general methods. N.d. = not determined.

b) Analysis of the phosphate and Amylose content

No.	Genotype	Phosphate in C6 (%)	Total phosphate in (%)	Amylose (%)	Amylose (% WT)
1	cv. Desiree	100,0	100,0	21,3	100,0
2	369SO048	72,8	84,8	20,8	97,7
3	369SO050	79,2	78,0	20,1	94,4
4	369SO052	84,8	83,2	19,6	92,0
5	369SO106	84,8	85,9	20,1	94,4
6	369SO129	80,8	81,2	20,2	94,8

Table 3: Phosphate and amylose contents of starch isolated from wild-type plants (cv. Desiree), plants with a reduced activity of BEIII protein (369SO). The phosphate contents in the C6 position of the glucose monomers and the total phosphate content of the starch are indicated in per cent based on starch from wild-type plants; amylose contents are indicated in per cent amylose based on the total amount of the starch, or in per cent based on the amylose content of starch from wild-type plants.

c) Analysis of side-chain distribution

- 10 The analysis of the side-chain distribution of the amylopectin was carried out as described above. The table which follows is a summary of the contributions of the individual peak areas:

Glucose units	cv. Desiree	369SO 048	369SO 050	369SO 052	369SO 106	369SO 129
dp 6	2,19	2,57	2,83	2,78	2,59	2,59
dp 7	1,69	1,76	1,84	1,85	1,85	1,73
dp 8	1,35	1,34	1,37	1,38	1,44	1,36
dp 9	2,26	2,27	2,31	2,32	2,42	2,31
dp 10	3,74	3,81	3,86	3,94	4,00	3,85
dp 11	5,13	5,23	5,30	5,45	5,37	5,30
dp 12	5,99	6,14	6,18	6,32	6,17	6,17
dp 13	6,40	6,53	6,54	6,63	6,48	6,63
dp 14	6,39	6,45	6,44	6,49	6,37	6,52
dp 15	6,11	6,14	6,12	6,15	6,05	6,09
dp 16	5,74	5,75	5,72	5,75	5,68	5,72
dp 17	5,37	5,35	5,35	5,35	5,30	5,35
dp 18	5,08	5,04	5,06	5,05	5,01	5,06
dp 19	4,89	4,86	4,88	4,84	4,83	4,86
dp 20	4,68	4,59	4,65	4,60	4,60	4,62

Glucose units	cv. Desiree	369SO 048	369SO 050	369SO 052	369SO 106	369SO 129
dp 6	100	117,4	129,2	126,9	118,3	118,3
dp 7	100	104,1	108,9	109,5	109,5	102,4
dp 8	100	99,3	101,5	102,2	106,7	100,7
dp 9	100	100,7	102,4	102,9	107,3	102,4
dp 10	100	102,0	103,3	105,5	107,1	103,1
dp 11	100	102,0	103,4	106,3	104,8	103,4
dp 12	100	102,5	103,2	105,5	103,0	103,0
dp 13	100	102,1	102,3	103,7	101,3	103,7
dp 14	100	100,9	100,8	101,6	99,7	102,0
dp 15	100	100,5	100,2	100,7	99,0	99,7
dp 16	100	100,3	99,7	100,3	99,0	99,7
dp 17	100	99,7	99,7	99,7	98,8	99,7
dp 18	100	99,3	99,7	99,5	98,7	99,7
dp 19	100	99,5	99,9	99,1	98,9	99,5
dp 20	100	98,1	99,4	98,3	98,3	98,7
dp 21	100	99,5	99,1	98,0	98,4	98,6
dp 22	100	98,8	99,0	97,6	98,0	98,0
dp 23	100	98,8	97,7	96,2	98,3	98,8
dp 24	100	98,4	96,9	96,0	98,1	96,9
dp 25	100	96,9	95,9	94,0	96,6	97,2
dp 26	100	97,1	94,2	93,5	96,4	95,6
dp 27	100	95,8	93,8	91,7	95,0	95,0
dp 28	100	96,1	92,3	91,3	95,2	93,7
dp 29	100	97,2	92,0	90,3	95,5	94,9
dp 30	100	94,0	91,4	89,4	93,4	93,4
dp 31	100	95,6	90,8	89,2	92,4	94,0
dp 32	100	94,2	89,3	89,3	92,2	92,2
dp 33	100	92,2	89,8	91,0	93,4	93,4
dp 34	100	91,9	88,9	90,4	93,3	91,9

Table 5: The table shows a summary of the contributions of the individual peak areas of the HPAEC chromatogram in per cent based on starch from wild-type plants.

5 d) Analysis of the amylopectin side chain distribution by means of gel permeation chromatography

Analysis of the amylopectin side chain distribution by means of gel permeation chromatography were additionally performed.

To separate amylose and amylopectin, 100 mg of starch are dissolved in 6 ml of 90% strength (v/v) DMSO with constant stirring. After addition of 3 volumes of ethanol, the precipitate is separated off by centrifugation for 10 minutes at 1800xg at room temperature. The pellet is subsequently washed with 30 ml of ethanol, dried and dissolved in 10 ml of 1% strength (w/v) NaCl solution at 60°C. After cooling the

solution to 30°C, approximately 50 mg of thymol are added slowly, and this solution is incubated for 2 to 3 days at 30°C. The solution is subsequently centrifuged for 30 minutes at 2000xg at room temperature. The supernatant is treated with three volumes of ethanol, and the amylopectin which precipitates is separated off by
5 centrifugation for 5 minutes at 2000xg at room temperature. The pellet (amylopectin) is washed with 10 ml of 70% strength (v/v) ethanol, centrifuged for 10 minutes at 2000xg at room temperature and then dried using acetone.

10 mg of amylopectin are subsequently stirred for 10 minutes at 70°C in 250 µl of 90% strength (v/v) DMSO. 375 µl of water at a temperature of 80°C are added to the
10 solution until dissolution is complete.

200 µl of this solution are treated with 300 µl of a 16.6 mM sodium acetate solution pH 3.5 and 2 µl of isoamylase (0.24 u/µl, Megazyme, Sydney, Australia) and the mixture is incubated for 15 hours at 37°C.

A 1:4 dilution of this aqueous isoamylase reaction mixture with DMSO, comprising
15 90 mM sodium nitrate, is subsequently filtered through a 0.2 µm filter, and 24 µl of the filtrate is analysed chromatographically. Separation was carried out with two columns connected in series, first a Gram PSS3000 (Polymer Standards Service, with suitable precolumn), followed by a Gram PSS100. Detection was by means of refraction index detector (RI 71, Shodex). The column was equilibrated with DMSO
20 comprising 90 mM sodium nitrate. It was eluted with DMSO comprising 90 mM sodium nitrate at a flow rate of 0.7 ml/min over a period of 1 hour.

To correlate the elution volume with the molecular mass, the column used was calibrated with dextran standards. The dextrans used, their molecular mass and the elution volumes are shown in Table 6. Using the resulting calibration graph, the
25 elution diagram was pictured as a molecular weight distribution.

The chromatograms obtained were further evaluated using the program Wingpc Version 6 from Polymer Standards Service GmbH, Mainz, Germany.

The total area under the line of the GPC chromatogram was divided into individual segments, each of which represent groups of side chains of different lengths. The
30 chosen segments contained glucan chains with the following degree of polymerization (DP = number of glucose monomers within one side chain): DP<12, DP12-18, DP19-24, DP25-30, DP31-36, DP37-42, DP43-48, DP49-55, DP56-61 and DP62-123. To determine the molecular weight of the individual side chains, a

molecular weight of 162 was assumed for glucose. The total area under the line in the GPC chromatogram was then set as 100%, and the percentage of the areas of the individual segments was calculated based on the percentage of the total area. Results obtained from this analysis are shown in Table 7.

5

elution volume [ml]	molar mass [D]	sample
18,76	401300	Dextran T670
19,41	276500	Dextran T410
20,49	196300	Dextran T270
21,35	123600	Dextran T150
22,45	66700	Dextran T80
23,52	43500	Dextran T50
25,15	21400	Dextran T25
26,92	9890	Dextran T12
28,38	4440	Dextran T5
30,77	1080	Dextran T1

Table 6: Calibration table.

degree of polymerisation	% total area					
	cv.Desiree	369 SO 48	369 SO 50	369 SO 52	369 SO 106	369 SO 129
<dp12	16,49	16,57	17,07	17,73	17,59	17,64
dp12-19	13,89	14,47	14,22	14,82	14,16	14,23
dp20-25	15,74	16,54	16,15	16,74	16,32	16,51
dp26-31	9,41	9,73	9,57	9,80	9,86	9,88
dp32-37	8,53	8,53	8,45	8,56	8,59	8,45
dp38-43	6,82	6,67	6,57	6,63	6,58	6,44
dp44-49	6,05	5,91	5,81	5,83	5,79	5,72
dp50-56	4,88	4,78	4,71	4,66	4,70	4,67
dp57-62	4,26	4,15	4,10	3,98	4,09	4,10
dp63-123	13,92	12,66	13,35	11,25	12,31	12,38

- 10 Table 7: Side chain profiles DP<12, DP 12 to 18, DP 19 to 24, DP 25 to 30, DP 31 to 36, DP 37 to 42, DP 43-48, DP 49 to 55, DP 56 to 61 and DP 62 to 123 for amylopectin isolated from wild-type plants (cv. Desiree) and from plants with a reduced activity of a BEIII protein (369SO).

degree of polymerisation	% WT					
	cv.Desiree	369 SO 48	369 SO 50	369 SO 52	369 SO 106	369 SO 129
<dp12	100,00	100,47	103,53	107,53	106,69	106,96
dp12-19	100,00	104,13	102,37	106,68	101,90	102,40
dp20-25	100,00	105,11	102,62	106,32	103,69	104,87
dp26-31	100,00	103,34	101,67	104,09	104,81	104,92
dp32-37	100,00	100,01	99,05	100,38	100,73	99,04
dp38-43	100,00	97,74	96,40	97,23	96,54	94,48
dp44-49	100,00	97,68	96,00	96,27	95,76	94,48
dp50-56	100,00	97,90	96,45	95,57	96,28	95,78
dp57-62	100,00	97,36	96,07	93,44	95,91	96,13
dp63-123	100,00	90,95	95,89	80,82	88,41	88,89

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Table 8: Side chain profiles DP<12, DP 12 to 18, DP 19 to 24, DP 25 to 30, DP 31 to 36, DP 37 to 42, DP 43-48, DP 49 to 55, DP 56 to 61 and DP 62 to 123 for

amylopectin isolated from wild-type plants (cv. Desiree) and from plants with a reduced activity of a BEIII protein (369SO). The percentages indicate the modification of the individual side chain profiles based on amylopectin isolated from wild-type plants.

5

e) DSC-analysis („Differential Scanning Calorimetry“)

Investigations with the aid of DSC-analysis („Differential Scanning Calorimetry“) have been done by the method described by WO 01/19975. Results obtained from this

10 analysis are shown in Table 9.

	T0 (°C)	T0 (%)	T Peak (°C)	T Peak (%)	dH (J/g)	dH (J/g)
cv.Desiree	64,84	100	68,09	100	20,31	100
369SO048	64,32	99,2	67,16	98,6	20,33	100,1
369SO050	63,35	97,7	66,75	98,0	20,63	101,6
369SO052	63,27	97,6	66,46	97,6	21,23	104,5
369SO106	63,77	98,3	66,96	98,3	21,42	105,5
369SO129	63,75	98,3	67,41	99,0	20,57	101,3

Table 9: Parameters of the DSC analysis of starch isolated from wild-type plants (cv. Desiree), plants with a reduced activity of a BEIII protein (369SO) indicated in °C respectively J/g and in per cent based on data of starch of the wild type. The DSC analysis was carried out as described in general methods. T0 [°C] = peak onset, T Peak [°C] = Peak temperature, dH [J/g] = heat of melting.

15

Patent claims

1. Genetically modified plant cell, characterised in that it has a reduced activity of at least one Class 3 branching enzyme in comparison with corresponding wild type plant cells that have not been genetically modified.
2. Genetically modified plant cell according to Claim 1, wherein the genetic modification consists in the introduction of at least one foreign nucleic acid molecule into the genome of the plant cell.
3. Genetically modified plant cell according to Claim 2, wherein the foreign nucleic acid molecule codes a Class 3 branching enzyme.
4. Genetically modified plant cell according to Claim 3, wherein the said foreign nucleic acid molecule is chosen from the group consisting of
 - a) Nucleic acid molecules, which code a protein with the amino acid sequence given under Seq ID No. 4;
 - b) Nucleic acid molecules, which code a protein, the amino acid sequence of which has an identity of at least 50% with the amino acid sequence given under SEQ ID NO: 4;
 - c) Nucleic acid molecules, which include the nucleotide sequence shown under Seq ID No. 3 or a complimentary sequence;
 - d) Nucleic acid molecules, the nucleic acid sequence of which has an identity of at least 50% with the nucleic acid sequences described under a) or c);
 - e) Nucleic acid molecules, which hybridise with at least one strand of the nucleic acid molecules described under a) or c) under stringent conditions;
 - f) Nucleic acid molecules, the nucleotide sequence of which deviates from the sequence of the nucleic acid molecules identified under a), b), c), d), e) or f) due to the degeneration of the genetic code; and

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- g) Nucleic acid molecules, which represent fragments, allelic variants and/or derivatives of the nucleic acid molecules identified under a), b), c), d), e) or f).
5. Genetically modified plant cell according to one of Claims 2, 3 or 4, wherein the said foreign nucleic acid molecule is chosen from the group consisting of
- a) DNA molecules, which code at least one antisense RNA, which effects a reduction in the expression of at least one endogenous gene, which codes a Class 3 branching enzyme;
 - b) DNA molecules, which by means of a co-suppression effect lead to the reduction in the expression of at least one endogenous gene, which codes a Class 3 branching enzyme;
 - c) DNA molecules, which code at least one ribozyme, which splits specific transcripts of at least one endogenous gene, which codes a Class 3 branching enzyme;
 - d) DNA molecules, which simultaneously code at least one antisense RNA and at least one sense RNA, wherein the said antisense RNA and the said sense RNA form a double-stranded RNA molecule, which effects a reduction in the expression of at least one endogenous gene, which codes a Class 3 branching enzyme (RNAi technology);
 - e) Nucleic acid molecules introduced by means of in vivo mutagenesis, which lead to a mutation or an insertion of a heterologous sequence in at least one endogenous gene coding a Class 3 branching enzyme, wherein the mutation or insertion effects a reduction in the expression of a gene coding a Class 3 branching enzyme or results in the synthesis of inactive Class 3 branching enzymes;
 - f) Nucleic acid molecules, which code an antibody, wherein the antibody results in a reduction in the activity of a Class 3 branching enzyme due to the bonding to a Class 3 branching enzyme.
 - g) DNA molecules, which contain transposons, wherein the integration of these transposons leads to a mutation or an insertion in at least one endogenous

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gene coding a Class 3 branching enzyme, which effects a reduction in the expression of at least one gene coding a Class 3 branching enzyme, or results in the synthesis of inactive Class 3 branching enzymes; and/or

- h) T-DNA molecules, which, due to insertion in at least one endogenous gene coding a Class 3 branching enzyme, effect a reduction in the expression of at least one gene coding a Class 3 branching enzyme, or result in the synthesis of inactive Class 3 branching enzyme.
6. Plant cell according to one of Claims 1 to 5, which synthesises a modified starch in comparison with corresponding wild type plant cells that have not been genetically modified.
 7. Plant containing plant cells according to one of Claims 1 to 6.
 8. Plant according to Claim 7, which is a starch-storing plant.
 9. Plant according to Claim 8, which is a maize, rice, wheat, rye, oat, barley, cassava, potato, sago, mung bean, pea or sorghum plant.
 10. Plant according to Claim 8, which is a potato plant.
 11. Propagation material of plants according to one of Claims 7 to 10, containing plant cells according to one of Claims 1 to 6.
 12. Harvestable plant parts of plants according to one of Claims 7 to 10, containing plant cells according to one of Claims 1 to 6.
 13. Method for the manufacture of a genetically modified plant according to one of Claims 7 to 10, wherein
 - a) a plant cell is genetically modified, whereby the genetic modification leads to the reduction of the activity of a Class 3 vegetable branching enzyme in comparison with corresponding wild type plant cells that have not been genetically modified;
 - b) a plant is regenerated from plant cells from Step a); and

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- c) if necessary, further plants are produced with the help of the plants according to Step b).
14. Method according to Claim 13, wherein the genetic modification consists in the introduction of at least one foreign nucleic acid molecule into the genome of the plant.
15. Method according to Claim 14, wherein the said foreign nucleic acid molecule is chosen from the group consisting of
- a) Nucleic acid molecules, which code a protein with the amino acid sequence given under Seq ID No. 4;
 - b) Nucleic acid molecules, which code a protein, the amino acid sequence of which has an identity of at least 50% with the amino acid sequence given under SEQ ID NO: 4;
 - c) Nucleic acid molecules, which include the nucleotide sequence shown under Seq ID No. 3 or a complimentary sequence;
 - d) Nucleic acid molecules, the nucleic acid sequence of which has an identity of at least 50% with the nucleic acid sequences described under a) or c);
 - e) Nucleic acid molecules, which hybridise with at least one strand of the nucleic acid molecules described under a) or c) under stringent conditions;
 - f) Nucleic acid molecules, the nucleotide sequence of which deviates from the sequence of the nucleic acid molecules identified under a), b), c), d), e) or f) due to the degeneration of the genetic code; and
 - g) Nucleic acid molecules, which represent fragments, allelic variants and/or derivatives of the nucleic acid molecules identified under a), b), c), d), e) or f).
16. Method according to Claim 14, wherein the said foreign nucleic acid molecule is chosen from the group consisting of

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- a) DNA molecules, which code at least one antisense RNA, which effects a reduction in the expression of at least one endogenous gene, which codes a Class 3 branching enzyme;
- b) DNA molecules, which by means of a co-suppression effect lead to the reduction in the expression of at least one endogenous gene, which codes a Class 3 branching enzyme;
- c) DNA molecules, which code at least one ribozyme, which splits specific transcripts of at least one endogenous gene, which codes a Class 3 branching enzyme;
- d) DNA molecules, which simultaneously code at least one antisense RNA and at least one sense RNA, wherein the said antisense RNA and the said sense RNA form a double-stranded RNA molecule, which effects a reduction in the expression of at least one endogenous gene, which codes a Class 3 branching enzyme (RNAi technology);
- e) Nucleic acid molecules introduced by means of in vivo mutagenesis, which lead to a mutation or an insertion of a heterologous sequence in at least one endogenous gene coding a Class 3 branching enzyme, wherein the mutation or insertion effects a reduction in the expression of a gene coding a Class 3 branching enzyme or results in the synthesis of inactive Class 3 branching enzymes;
- f) Nucleic acid molecules, which code an antibody, wherein the antibody results in a reduction in the activity of a Class 3 branching enzyme due to the bonding to a Class 3 branching enzyme.
- g) DNA molecules, which contain transposons, wherein the integration of these transposons leads to a mutation or an insertion in at least one endogenous gene coding a Class 3 branching enzyme, which effects a reduction in the expression of at least one gene coding a Class 3 branching enzyme, or results in the synthesis of inactive Class 3 branching enzymes; and/or

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- h) T-DNA molecules, which, due to insertion in at least one endogenous gene coding a Class 3 branching enzyme, effect a reduction in the expression of at least one gene coding a Class 3 branching enzyme, or result in the synthesis of inactive Class 3 branching enzyme.
17. Method according to one of Claims 13 to 17 [sic], wherein the genetically modified plant synthesises a modified starch in comparison with corresponding wild type plants that have not been genetically modified.
18. Nucleic acid molecule, coding for a protein with the enzymatic activity of a Class 3 branching enzyme, chosen from the group consisting of
- a) Nucleic acid molecules, which code a protein with the amino acid sequence given under Seq ID No. 4;
 - b) Nucleic acid molecules, which code a protein, the amino acid sequence of which has an identity of at least 70% with the amino acid sequence given under SEQ ID NO: 4;
 - c) Nucleic acid molecules, which include the nucleotide sequence shown under Seq ID No. 3 or a complimentary sequence;
 - d) Nucleic acid molecules, which have an identity of at least 70% with the nucleic acid sequences described under a) or c);
 - e) Nucleic acid molecules, which hybridise with at least one strand of the nucleic acid molecules described under a) or c) under stringent conditions;
 - f) Nucleic acid molecules, the nucleotide sequence of which deviates from the sequence of the nucleic acid molecules identified under a), b), c), d), e) or f) due to the degeneration of the genetic code; and
 - g) Nucleic acid molecules, which represent fragments, allelic variants and/or derivatives of the nucleic acid molecules identified under a), b), c), d), e) or f).
19. Nucleic acid molecule according to Claim 18, characterised in that it codes a Class 3 branching enzyme of potato.

20. Vector containing a nucleic acid molecule according to one of Claims 18 or 19.
21. Vector according to Claim 20, wherein the nucleic acid molecule is linked with regulatory sequences, which guarantee transcription into prokaryotic or eukaryotic cells.
22. Vector containing a foreign nucleic acid molecule defined as in Claim 5 under a), b), c) or d).
23. Host cell, which is genetically modified with a nucleic acid molecule according to one of Claims 18 or 19 or with a vector according to one of Claims 20, 21 or 22.
24. Protein with the enzymatic activity of a Class 3 branching enzyme, chosen from the group consisting of
 - a) Proteins, which include the amino acid sequence specified under SEQ ID No. 4, or
 - b) Proteins, which have an identity of at least 70% with the amino acid sequence of the proteins identified under a).
25. Protein according to Claim 24, wherein the Class 3 branching enzyme comes from a potato plant.
26. Modified starch obtainable from a genetically modified plant according to one of Claims 7 to 10, from propagation material according to Claim 11, or from harvestable plant parts according to Claim 12.
27. Method for the manufacture of a modified starch including the step of extracting the starch from a plant cell according to one of Claims 1 to 6.
28. Method for the manufacture of a modified starch including the step of extracting the starch from a plant according to one of Claims 7 to 10, and/or from starch-storing parts of such a plant.
29. Method for the manufacture of a modified starch including the step of extracting the starch from harvestable plant parts according to Claim 12.

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30. Method for the manufacture of a derived starch, wherein modified starch according to Claim 26 or obtainable by means of a method according to one of Claims 27, 28 or 29 is derived.
31. Use of genetically modified plants according to one of Claims 7 to 10 for the manufacture of a modified starch.
32. Modified starch obtainable by means of a method according to one of Claims 27, 28 or 29.
33. Derived starch obtainable by means of a method according to Claim 30.
34. Use of modified starch according to one of Claims 26 or 32 for the manufacture of derived starch.

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 acaaattatt ggagttgttg agcacaagga ttatttact gttggatata gagtgaacaa 1380
 tttttatgct gttagtagcc gttatggcac accggatgac ttcaagcgct tgggtgatga 1440
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<220>
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<222> (99)..(2804)
<223>

[illegible]

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Thr	His	Lys	Ala	Phe	Ala	Gln	Phe	Leu	Arg	Glu	Arg	Tyr	Lys	Ser	Leu	
		90						95					100			
aag	gac	ttg	aag	gat	gaa	ata	ttg	act	cgt	cat	ttc	agt	ctc	aag	gag	452
Lys	Asp	Leu	Lys	Asp	Glu	Ile	Leu	Thr	Arg	His	Phe	Ser	Leu	Lys	Glu	
		105					110					115				
atg	tct	act	ggg	tat	gaa	tta	atg	ggg	atg	cat	cgc	aac	ata	caa	cat	500
Met	Ser	Thr	Gly	Tyr	Glu	Leu	Met	Gly	Met	His	Arg	Asn	Ile	Gln	His	
	120					125					130					
cga	gtg	gat	ttc	ttg	gaa	tgg	gct	cca	ggg	gct	cgc	tac	tgt	gct	ctg	548
Arg	Val	Asp	Phe	Leu	Glu	Trp	Ala	Pro	Gly	Ala	Arg	Tyr	Cys	Ala	Leu	
135					140					145					150	
att	ggg	gac	ttc	aat	ggg	tgg	tca	aca	act	ggg	aac	tgt	gcc	aga	gag	596
Ile	Gly	Asp	Phe	Asn	Gly	Trp	Ser	Thr	Thr	Gly	Asn	Cys	Ala	Arg	Glu	
				155					160					165		
ggg	cat	ttt	ggg	cat	gac	gat	tat	ggg	tat	tgg	ttt	att	att	ctt	gaa	644
Gly	His	Phe	Gly	His	Asp	Asp	Tyr	Gly	Tyr	Trp	Phe	Ile	Ile	Leu	Glu	
			170					175					180			
gat	aaa	tta	cgt	gaa	gga	gaa	gaa	cct	gat	aaa	ttg	tat	ttt	caa	cag	692
Asp	Lys	Leu	Arg	Glu	Gly	Glu	Glu	Pro	Asp	Lys	Leu	Tyr	Phe	Gln	Gln	
		185					190					195				
tac	aat	tat	gcg	gag	gac	tat	gat	aaa	ggg	gac	acg	ggg	att	acc	gtc	740
Tyr	Asn	Tyr	Ala	Glu	Asp	Tyr	Asp	Lys	Gly	Asp	Thr	Gly	Ile	Thr	Val	
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gag	gaa	atc	ttt	aaa	aaa	gca	aat	gat	gag	tat	tgg	gaa	cct	gga	gaa	788
Glu	Glu	Ile	Phe	Lys	Lys	Ala	Asn	Asp	Glu	Tyr	Trp	Glu	Pro	Gly	Glu	
215					220					225					230	
gat	cgc	ttc	att	aaa	tca	cgt	tat	gag	gtg	gca	gca	aag	tta	tat	gag	836
Asp	Arg	Phe	Ile	Lys	Ser	Arg	Tyr	Glu	Val	Ala	Ala	Lys	Leu	Tyr	Glu	
				235					240					245		
gaa	atg	ttc	gga	cca	aat	gga	cct	caa	aca	gaa	gag	gaa	cta	gaa	gca	884
Glu	Met	Phe	Gly	Pro	Asn	Gly	Pro	Gln	Thr	Glu	Glu	Glu	Leu	Glu	Ala	
			250					255					260			
atg	cct	gat	gca	gct	aca	cga	tac	aaa	act	tgg	aaa	gag	caa	caa	aaa	932
Met	Pro	Asp	Ala	Ala	Thr	Arg	Tyr	Lys	Thr	Trp	Lys	Glu	Gln	Gln	Lys	
		265					270					275				
aag	gat	ccg	gca	agc	aat	ttg	cca	tcg	tat	gat	gtg	gta	gat	agt	gga	980
Lys	Asp	Pro	Ala	Ser	Asn	Leu	Pro	Ser	Tyr	Asp	Val	Val	Asp	Ser	Gly	
	280					285					290					
aaa	gaa	tat	gat	att	tac	aat	att	ata	ggg	gat	cct	gaa	tcg	ttt	aag	1028
Lys	Glu	Tyr	Asp	Ile	Tyr	Asn	Ile	Ile	Gly	Asp	Pro	Glu	Ser	Phe	Lys	
295					300					305					310	
aaa	ttt	cgt	atg	aaa	cag	cct	cct	att	gct	tac	tgg	tta	gaa	act	aaa	1076
Lys	Phe	Arg	Met	Lys	Gln	Pro	Pro	Ile	Ala	Tyr	Trp	Leu	Glu	Thr	Lys	
				315					320					325		
aag	gga	agg	aaa	ggc	tgg	tta	cag	aaa	tat	atg	cct	gct	tta	cct	cat	1124
Lys	Gly	Arg	Lys	Gly	Trp	Leu	Gln	Lys	Tyr	Met	Pro	Ala	Leu	Pro	His	
			330					335					340			
gga	agc	aaa	cac	agg	gtg	tat	ttt	aac	aca	cca	aat	ggg	cct	ctt	gaa	1172
Gly	Ser	Lys	His	Arg	Val	Tyr	Phe	Asn	Thr	Pro	Asn	Gly	Pro	Leu	Glu	
		345					350					355				

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cga gtt cct gcg tgg gcc aat ttt gtc att cca gat gca gac ggg atg Arg Val Pro Ala Trp Ala Asn Phe Val Ile Pro Asp Ala Asp Gly Met 360 365 370	1220
gca tta gca gtc cat tgg gaa cca cct cct gaa tat gct tat aaa tgg Ala Leu Ala Val His Trp Glu Pro Pro Pro Glu Tyr Ala Tyr Lys Trp 375 380 385 390	1268
aaa cac aag cta cca gtc aag cct aag tcc ttg cgc ata tat gaa tgt Lys His Lys Leu Pro Val Lys Pro Lys Ser Leu Arg Ile Tyr Glu Cys 395 400 405	1316
cat gtt ggc atc tct ggc cag gaa cca aaa gtt tca tct ttc aat gat His Val Gly Ile Ser Gly Gln Glu Pro Lys Val Ser Ser Phe Asn Asp 410 415 420	1364
ttt att agc aag gtc ctt ccg cat gta aaa gaa gct gga tac aat gca Phe Ile Ser Lys Val Leu Pro His Val Lys Glu Ala Gly Tyr Asn Ala 425 430 435	1412
acg caa att att gga gtt gtt gag cac aag gat tat ttc act gtt gga Thr Gln Ile Ile Gly Val Val Glu His Lys Asp Tyr Phe Thr Val Gly 440 445 450	1460
tat aga gtg acc aat ttt tat gct gtt agt agc cgt tat ggc aca ccg Tyr Arg Val Thr Asn Phe Tyr Ala Val Ser Ser Arg Tyr Gly Thr Pro 455 460 465 470	1508
gat gac ttc aag cgc ttg gtt gat gaa gca cat ggg ctt gga ctg ctt Asp Asp Phe Lys Arg Leu Val Asp Glu Ala His Gly Leu Gly Leu Leu 475 480 485	1556
gtc ttt ttg gag att gtg cac tcc tat gca gca gca gat gaa atg gtt Val Phe Leu Glu Ile Val His Ser Tyr Ala Ala Ala Asp Glu Met Val 490 495 500	1604
ggg tta tct ctt ttt gat gga gca aat gat tgc tat ttc cac act ggt Gly Leu Ser Leu Phe Asp Gly Ala Asn Asp Cys Tyr Phe His Thr Gly 505 510 515	1652
aaa cgt gga cac cac aaa ttc tgg ggc aca cgg atg ttc aaa tat gga Lys Arg Gly His His Lys Phe Trp Gly Thr Arg Met Phe Lys Tyr Gly 520 525 530	1700
gat cct gat gtt ctg cac ttt ctt ctt tca aat ctg aac tgg tgg gtg Asp Pro Asp Val Leu His Phe Leu Leu Ser Asn Leu Asn Trp Trp Val 535 540 545 550	1748
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tac tgt aac caa tat gtt gac aag gag gcc tta ttg tac ctc ata tta Tyr Cys Asn Gln Tyr Val Asp Lys Glu Ala Leu Leu Tyr 585 590 595	1892
gca aat gaa gta tta cat gct ctt cat cct aat gtg atc acg att gct Ala Asn Glu Val Leu His Ala Leu His Pro Asn Val Ile Thr Ile Ala 600 605 610	1940
gtg gat gca act ctg tat cct gga ctc tgc gat cca aca tct caa ggt Val Asp Ala Thr Leu Tyr Pro Gly Leu Cys Asp Pro Thr Ser Gln Gly 615 620 625 630	1988

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Gly	Leu	Gly	Phe	Asp	Tyr	Phe	Ala	Asn	Leu	Ser	Ala	Ser	Glu	Met	Trp	
				635					640					645		
ctt	gca	tta	ctt	gaa	aat	act	cct	gat	cat	gaa	tgg	tgc	atg	agt	aag	2084
Leu	Ala	Leu	Leu	Glu	Asn	Thr	Pro	Asp	His	Glu	Trp	Cys	Met	Ser	Lys	
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att	gtt	agc	aca	tta	gtg	ggc	gat	aga	caa	aat	act	gat	aaa	atg	ctt	2132
Ile	Val	Ser	Thr	Leu	Val	Gly	Asp	Arg	Gln	Asn	Thr	Asp	Lys	Met	Leu	
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Leu	Tyr	Ala	Glu	Asn	His	Asn	Gln	Ser	Ile	Ser	Gly	Gly	Arg	Ser	Phe	
	680					685					690					
gca	gaa	ata	ctg	att	ggt	aac	tcc	ttg	ggg	aaa	tct	tcc	ata	tca	caa	2228
Ala	Glu	Ile	Leu	Ile	Gly	Asn	Ser	Leu	Gly	Lys	Ser	Ser	Ile	Ser	Gln	
	695				700					705					710	
gag	tca	tta	ctt	aga	ggc	tgc	tgc	tta	cac	aag	atg	atc	aga	tta	att	2276
Glu	Ser	Leu	Leu	Arg	Gly	Cys	Ser	Leu	His	Lys	Met	Ile	Arg	Leu	Ile	
				715					720					725		
aca	tct	aca	att	ggt	ggt	cat	gca	tac	ctc	aac	ttc	atg	ggc	aat	gaa	2324
Thr	Ser	Thr	Ile	Gly	Gly	His	Ala	Tyr	Leu	Asn	Phe	Met	Gly	Asn	Glu	
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ttt	ggt	cac	cca	aag	aga	gta	gag	ttt	cca	atg	tca	agc	aac	aat	ttc	2372
Phe	Gly	His	Pro	Lys	Arg	Val	Glu	Phe	Pro	Met	Ser	Ser	Asn	Asn	Phe	
		745					750					755				
tcc	ttt	tca	ctg	gct	aac	cgt	cgc	tgg	gat	cta	ttg	gaa	gat	gtt	gta	2420
Ser	Phe	Ser	Leu	Ala	Asn	Arg	Arg	Trp	Asp	Leu	Leu	Glu	Asp	Val	Val	
	760					765					770					
cat	tat	caa	tta	ttc	tca	ttt	gat	aag	gat	atg	atg	gac	ttg	gat	aaa	2468
His	Tyr	Gln	Leu	Phe	Ser	Phe	Asp	Lys	Asp	Met	Met	Asp	Leu	Asp	Lys	
	775				780					785					790	
aat	ggg	aga	att	ttg	tcc	aga	ggt	ctt	gcc	aac	att	cac	cat	gtc	aat	2516
Asn	Gly	Arg	Ile	Leu	Ser	Arg	Gly	Leu	Ala	Asn	Ile	His	His	Val	Asn	
				795					800					805		
gat	act	acc	atg	gtg	att	tct	tac	ttg	aga	ggt	ccc	aat	ctc	ttt	gtg	2564
Asp	Thr	Thr	Met	Val	Ile	Ser	Tyr	Leu	Arg	Gly	Pro	Asn	Leu	Phe	Val	
			810					815					820			
ttc	aac	ttt	cat	cct	gtc	aat	tca	tat	gaa	aga	tac	att	ata	ggt	gtg	2612
Phe	Asn	Phe	His	Pro	Val	Asn	Ser	Tyr	Glu	Arg	Tyr	Ile	Ile	Gly	Val	
		825					830					835				
gaa	gaa	gct	gga	gag	tat	caa	gtc	aca	tta	aat	aca	gat	gaa	aac	aag	2660
Glu	Glu	Ala	Gly	Glu	Tyr	Gln	Val	Thr	Leu	Asn	Thr	Asp	Glu	Asn	Lys	
	840					845					850					
tat	ggt	ggt	aga	gga	cta	ctt	ggc	cat	gat	cag	aat	act	caa	aga	acc	2708
Tyr	Gly	Gly	Arg	Gly	Leu	Leu	Gly	His	Asp	Gln	Asn	Thr	Gln	Arg	Thr	
	855				860					865					870	
att	agt	aga	aga	gct	gat	gga	atg	aga	ttt	tgc	ttg	gaa	gta	cct	ctg	2756
Ile	Ser	Arg	Arg	Ala	Asp	Gly	Met	Arg	Phe	Cys	Leu	Glu	Val	Pro	Leu	
				875					880					885		
cca	agt	aga	agt	gct	cag	gtc	tac	aag	ttg	acc	cga	att	cta	aga	gca	2804
Pro	Ser	Arg	Ser	Ala	Gln	Val	Tyr	Lys	Leu	Thr	Arg	Ile	Leu	Arg	Ala	
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tgatcactct agcaatcaaa gtgcctcata tgatcacaca aaaggaagg ttctacattg 2864
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 ggctgttggc tagtcagtta tcatgaactt ttgccttcag catctggata agcgcttctc 2984
 ctgtgcaatg agggcatgga cgaaattttt ttggttcgtc atgggagtca aaagcatctg 3044
 ccagattaag atttcacagg cctcgagtaa aaccatcact tacttaggat acacaaacac 3104
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<211> 902

<212> PRT

<213> Solanum tuberosum

<400> 4

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Leu Lys Phe Val Arg Ser Arg Arg Ala Arg Val Ser Arg Cys Arg Cys
 35 40 45

Ser Ala Thr Glu Gln Pro Pro Pro Gln Arg Arg Lys Gln Arg Pro Glu
 50 55 60

Lys Tyr Lys Gln Ser Glu Glu Lys Gly Ile Asp Pro Val Gly Phe
 65 70 75 80

Leu Ser Lys Tyr Gly Ile Thr His Lys Ala Phe Ala Gln Phe Leu Arg
 85 90 95

Glu Arg Tyr Lys Ser Leu Lys Asp Leu Lys Asp Glu Ile Leu Thr Arg
 100 105 110

His Phe Ser Leu Lys Glu Met Ser Thr Gly Tyr Glu Leu Met Gly Met
 115 120 125

His Arg Asn Ile Gln His Arg Val Asp Phe Leu Glu Trp Ala Pro Gly
 130 135 140

Ala Arg Tyr Cys Ala Leu Ile Gly Asp Phe Asn Gly Trp Ser Thr Thr
 145 150 155 160

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Gly Asn Cys Ala Arg Glu Gly His Phe Gly His Asp Asp Tyr Gly Tyr
 165 170 175

Trp Phe Ile Ile Leu Glu Asp Lys Leu Arg Glu Gly Glu Glu Pro Asp
 180 185 190

Lys Leu Tyr Phe Gln Gln Tyr Asn Tyr Ala Glu Asp Tyr Asp Lys Gly
 195 200 205

Asp Thr Gly Ile Thr Val Glu Glu Ile Phe Lys Lys Ala Asn Asp Glu
 210 215 220

Tyr Trp Glu Pro Gly Glu Asp Arg Phe Ile Lys Ser Arg Tyr Glu Val
 225 230 235 240

Ala Ala Lys Leu Tyr Glu Glu Met Phe Gly Pro Asn Gly Pro Gln Thr
 245 250 255

Glu Glu Glu Leu Glu Ala Met Pro Asp Ala Ala Thr Arg Tyr Lys Thr
 260 265 270

Trp Lys Glu Gln Gln Lys Lys Asp Pro Ala Ser Asn Leu Pro Ser Tyr
 275 280 285

Asp Val Val Asp Ser Gly Lys Glu Tyr Asp Ile Tyr Asn Ile Ile Gly
 290 295 300

Asp Pro Glu Ser Phe Lys Lys Phe Arg Met Lys Gln Pro Pro Ile Ala
 305 310 315 320

Tyr Trp Leu Glu Thr Lys Lys Gly Arg Lys Gly Trp Leu Gln Lys Tyr
 325 330 335

Met Pro Ala Leu Pro His Gly Ser Lys His Arg Val Tyr Phe Asn Thr
 340 345 350

Pro Asn Gly Pro Leu Glu Arg Val Pro Ala Trp Ala Asn Phe Val Ile
 355 360 365

Pro Asp Ala Asp Gly Met Ala Leu Ala Val His Trp Glu Pro Pro Pro
 370 375 380

Glu Tyr Ala Tyr Lys Trp Lys His Lys Leu Pro Val Lys Pro Lys Ser
 385 390 395 400

Leu Arg Ile Tyr Glu Cys His Val Gly Ile Ser Gly Gln Glu Pro Lys
 405 410 415

Val Ser Ser Phe Asn Asp Phe Ile Ser Lys Val Leu Pro His Val Lys
 420 425 430

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Glu Ala Gly Tyr Asn Ala Thr Gln Ile Ile Gly Val Val Glu His Lys
 435 440 445

Asp Tyr Phe Thr Val Gly Tyr Arg Val Thr Asn Phe Tyr Ala Val Ser
 450 455 460

Ser Arg Tyr Gly Thr Pro Asp Asp Phe Lys Arg Leu Val Asp Glu Ala
 465 470 475 480

His Gly Leu Gly Leu Leu Val Phe Leu Glu Ile Val His Ser Tyr Ala
 485 490 495

Ala Ala Asp Glu Met Val Gly Leu Ser Leu Phe Asp Gly Ala Asn Asp
 500 505 510

Cys Tyr Phe His Thr Gly Lys Arg Gly His His Lys Phe Trp Gly Thr
 515 520 525

Arg Met Phe Lys Tyr Gly Asp Pro Asp Val Leu His Phe Leu Leu Ser
 530 535 540

Asn Leu Asn Trp Trp Val Glu Glu Tyr His Val Asp Gly Phe His Phe
 545 550 555 560

His Ser Leu Ser Ser Met Leu Tyr Thr His Asn Gly Phe Ala Ser Phe
 565 570 575

Thr Gly Asp Met Asp Glu Tyr Cys Asn Gln Tyr Val Asp Lys Glu Ala
 580 585 590

Leu Leu Tyr Leu Ile Leu Ala Asn Glu Val Leu His Ala Leu His Pro
 595 600 605

Asn Val Ile Thr Ile Ala Val Asp Ala Thr Leu Tyr Pro Gly Leu Cys
 610 615 620

Asp Pro Thr Ser Gln Gly Gly Leu Gly Phe Asp Tyr Phe Ala Asn Leu
 625 630 635 640

Ser Ala Ser Glu Met Trp Leu Ala Leu Leu Glu Asn Thr Pro Asp His
 645 650 655

Glu Trp Cys Met Ser Lys Ile Val Ser Thr Leu Val Gly Asp Arg Gln
 660 665 670

Asn Thr Asp Lys Met Leu Leu Tyr Ala Glu Asn His Asn Gln Ser Ile
 675 680 685

Ser Gly Gly Arg Ser Phe Ala Glu Ile Leu Ile Gly Asn Ser Leu Gly
 690 695 700

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Lys Ser Ser Ile Ser Gln Glu Ser Leu Leu Arg Gly Cys Ser Leu His
 705 710 715 720

Lys Met Ile Arg Leu Ile Thr Ser Thr Ile Gly Gly His Ala Tyr Leu
 725 730 735

Asn Phe Met Gly Asn Glu Phe Gly His Pro Lys Arg Val Glu Phe Pro
 740 745 750

Met Ser Ser Asn Asn Phe Ser Phe Ser Leu Ala Asn Arg Arg Trp Asp
 755 760 765

Leu Leu Glu Asp Val Val His Tyr Gln Leu Phe Ser Phe Asp Lys Asp
 770 775 780

Met Met Asp Leu Asp Lys Asn Gly Arg Ile Leu Ser Arg Gly Leu Ala
 785 790 795 800

Asn Ile His His Val Asn Asp Thr Thr Met Val Ile Ser Tyr Leu Arg
 805 810 815

Gly Pro Asn Leu Phe Val Phe Asn Phe His Pro Val Asn Ser Tyr Glu
 820 825 830

Arg Tyr Ile Ile Gly Val Glu Glu Ala Gly Glu Tyr Gln Val Thr Leu
 835 840 845

Asn Thr Asp Glu Asn Lys Tyr Gly Gly Arg Gly Leu Leu Gly His Asp
 850 855 860

Gln Asn Thr Gln Arg Thr Ile Ser Arg Arg Ala Asp Gly Met Arg Phe
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Cys Leu Glu Val Pro Leu Pro Ser Arg Ser Ala Gln Val Tyr Lys Leu
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Thr Arg Ile Leu Arg Ala
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<211> 3047

<212> DNA

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<221> CDS

<222> (5)..(2710)

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gat tct cgt ctt agt ttt cta tct caa acc gga agc aga acc agt cgc 97
Asp Ser Arg Leu Ser Phe Leu Ser Gln Thr 25 Gly Ser Arg Thr Ser Arg 30
20

cag ctt aaa ttt gtt cgc agc cgc cgg gct cga gtt tcg agg tgt aga 145
Gln Leu Lys Phe Val Arg Ser Arg Arg Ala Arg Val Ser Arg Cys Arg 45
35 40

tgc tca gca acg gag caa ccg cca ccg caa cga cgg aag caa cga ccg 193
Cys Ser Ala Thr Glu Gln Pro Pro Pro Gln Arg Arg Lys Gln Arg Pro 60
50 55

gag aag tac aaa cag tcg gag gaa ggg aaa gga atc gat cct gtt gga 241
Glu Lys Tyr Lys Gln Ser Glu Glu Gly Lys Gly Ile Asp Pro Val Gly 75
65 70

ttt ctc agc aaa tac ggc att act cat aaa gcg ttt gct caa ttt ctt 289
Phe Leu Ser Lys Tyr Gly Ile Thr His Lys Ala Phe Ala Gln Phe Leu 95
80 85 90

cgt gaa aga tat aaa tca ttg aag gac ttg aag gat gaa ata ttg act 337
Arg Glu Arg Tyr Lys Ser Leu Lys Asp Leu Lys Asp Glu Ile Leu Thr 110
100 105

cgt cat ttc agt ctc aag gag atg tct act ggg tat gaa tta atg ggt 385
Arg His Phe Ser Leu Lys Glu Met Ser Thr Gly Tyr Glu Leu Met Gly 125
115 120

atg cat cgc aac ata caa cat cga gtg gat ttc ttg gaa tgg gct cca 433
Met His Arg Asn Ile Gln His Arg Val Asp Phe Leu Glu Trp Ala Pro 140
130 135

ggt gct cgc tac tgt gct ctg att ggt gac ttc aat ggg tgg tca aca 481
Gly Ala Arg Tyr Cys Ala Leu Ile Gly Asp Phe Asn Gly Trp Ser Thr 155
145 150

act ggt aac tgt gcc aga gag ggt cat ttt ggt cat gac gat tat ggg 529
Thr Gly Asn Cys Ala Arg Glu Gly His Phe Gly His Asp Asp Tyr Gly 175
160 165 170

tat tgg ttt att att ctt gaa gat aaa tta cgt gaa gga gaa gaa cct 577
Tyr Trp Phe Ile Ile Leu Glu Asp Lys Leu Arg Glu Gly Glu Glu Pro 190
180 185

gat aaa ttg tat ttt caa cag tac aat tat gcg gag gac tat ggt aaa 625
Asp Lys Leu Tyr Phe Gln Gln Tyr Asn Tyr Ala Glu Asp Tyr Gly Lys 205
195 200

ggt gac acg ggt att acc gtc gag gaa atc ttt aaa aaa gca aat gat 673
Gly Asp Thr Gly Ile Thr Val Glu Glu Ile Phe Lys Lys Ala Asn Asp 220
210 215

gag tat tgg gaa cct gga gaa gat cgc ttc att aaa tca cgt tat gag 721
Glu Tyr Trp Glu Pro Gly Glu Asp Arg Phe Ile Lys Ser Arg Tyr Glu 235
225 230

gtg gca gca aag tta tat gag gaa atg ttc gga cca aat gga cct caa 769
Val Ala Ala Lys Leu Tyr Glu Glu Met Phe Gly Pro Asn Gly Pro Gln 255
240 245

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tat gat gtg gta gat agt gga aaa gaa tat gat att tac aat att ata Tyr Asp Val Val Asp Ser Gly Lys Glu Tyr Asp Ile Tyr Asn Ile Ile 290 295 300	913
ggt gat cct gaa tcg ttt aag aaa ttt cgt atg aaa cag cct cct att Gly Asp Pro Glu Ser Phe Lys Lys Phe Arg Met Lys Gln Pro Pro Ile 305 310 315	961
gct tac tgg tta gaa act aaa aag gga agg aaa ggc tgg tta cag aaa Ala Tyr Trp Leu Glu Thr Lys Lys Gly Arg Lys Gly Trp Leu Gln Lys 320 325 330 335	1009
tat atg cct gct tta cct cat gga agc aaa tac agg gtg tat ttt aac Tyr Met Pro Ala Leu Pro His Gly Ser Lys Tyr Arg Val Tyr Phe Asn 340 345 350	1057
aca cca aat ggg cct ctt gaa cga gtt cct gcg tgg gcc aat ttt gtc Thr Pro Asn Gly Pro Leu Glu Arg Val Pro Ala Trp Ala Asn Phe Val 355 360 365	1105
att cca gat gca ggc ggg atg gca tta gca gtc cat tgg gaa cca cct Ile Pro Asp Ala Gly Gly Met Ala Leu Ala Val His Trp Glu Pro Pro 370 375 380	1153
cct gaa tat gct tat aaa tgg aaa cac aag cta cca gtc aag cct aag Pro Glu Tyr Ala Tyr Lys Trp Lys His Lys Leu Pro Val Lys Pro Lys 385 390 395	1201
tcc ttg cgc ata tat gaa tgt cat gtt ggc atc tct ggc cag gaa cca Ser Leu Arg Ile Tyr Glu Cys His Val Gly Ile Ser Gly Gln Glu Pro 400 405 410 415	1249
aaa gtt tca tct ttc aat gat ttt att agc aag gtc ctt ccg cat gta Lys Val Ser Ser Phe Asn Asp Phe Ile Ser Lys Val Leu Pro His Val 420 425 430	1297
aaa gaa gct gga tac aat gca ata caa att att gga gtt gtt gag cac Lys Glu Ala Gly Tyr Asn Ala Ile Gln Ile Ile Gly Val Val Glu His 435 440 445	1345
aag gat tat ttc act gtt gga tat aga gtg acc aat ttt tat gct gtt Lys Asp Tyr Phe Thr Val Gly Tyr Arg Val Thr Asn Phe Tyr Ala Val 450 455 460	1393
agt agc cgt tat ggc aca ccg gat gac ttc aag cgc ttg gtt gat gaa Ser Ser Arg Tyr Gly Thr Pro Asp Asp Phe Lys Arg Leu Val Asp Glu 465 470 475	1441
gca cat ggg ctt gga ctg ctt gtc ttt ttg gag att gtg cac tct tat Ala His Gly Leu Gly Leu Leu Val Phe Leu Glu Ile Val His Ser Tyr 480 485 490 495	1489
gca gca gca gat gaa atg gtt ggg tta tct ctt ttt gat gga gca aat Ala Ala Ala Asp Glu Met Val Gly Leu Ser 500 505 510	1537
gat tgc tat ttc cac act ggt aaa cgt gga cac cac aaa ttc tgg ggc Asp Cys Tyr Phe His Thr Gly Lys Arg Gly His His Lys Phe Trp Gly 515 520 525	1585

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aca cgg atg ttc aaa tat gga gat ctt gat gtt ctg cac ttt ctt ctt Thr Arg Met Phe Lys Tyr Gly Asp Leu Asp Val Leu His Phe Leu Leu 530 535 540	1633
tca aat ctg aac tgg tgg gtg gag gag tat cat gtc gat ggc ttc cat Ser Asn Leu Asn Trp Trp Val Glu Glu Tyr His Val Asp Gly Phe His 545 550 555	1681
ttt cat tcg ctc tcg tcc atg ttg tat acg cat aat gga ttt gct tca Phe His Ser Leu Ser Ser Met Leu Tyr Thr His Asn Gly Phe Ala Ser 560 565 570 575	1729
ttt act ggt gac atg gat gaa tac tgt aac caa tat gtt gac aag gag Phe Thr Gly Asp Met Asp Glu Tyr Cys Asn Gln Tyr Val Asp Lys Glu 580 585 590	1777
gcc tta ttg tac ctc ata tta gca aat gaa gta tta cat gct ctt cat Ala Leu Leu Tyr Leu Ile Leu Ala Asn Glu Val Leu His Ala Leu His 595 600 605	1825
cct aat gtg atc acg att gct gag gat gca act ctg tat cct gga ctc Pro Asn Val Ile Thr Ile Ala Glu Asp Ala Thr Leu Tyr Pro Gly Leu 610 615 620	1873
tgc gat cca aca tct caa ggt gga ctg ggc ttt gat tat ttt gcc aat Cys Asp Pro Thr Ser Gln Gly Gly Leu Gly Phe Asp Tyr Phe Ala Asn 625 630 635	1921
ctt tct gcc tca gag atg tgg ctt gca tta ctt gaa aat act cct gat Leu Ser Ala Ser Glu Met Trp Leu Ala Leu Leu Glu Asn Thr Pro Asp 640 645 650 655	1969
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caa aat act gat aaa atg ctt ttg tat gca gaa aat cac aac cag tcc Gln Asn Thr Asp Lys Met Leu Leu Tyr Ala Glu Asn His Asn Gln Ser 675 680 685	2065
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ggg aaa tcc tcc ata tca caa gag tca tta ctt aga ggc tgc tcg tta Gly Lys Ser Ser Ile Ser Gln Glu Ser Leu Leu Arg Gly Cys Ser Leu 705 710 715	2161
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ctc aac ttc atg ggc aat gaa ttt ggt cac cca aag aga gta gag ttt Leu Asn Phe Met Gly Asn Glu Phe Gly His Pro Lys Arg Val Glu Phe 740 745 750	2257
cca atg tca agc aac aat ttc tcc ttt tca ctg gct aac cgt cgc tgg Pro Met Ser Ser Asn Asn Phe Ser Phe Ser Leu Ala Asn Arg Arg Trp 755 760 765	2305
gat cta ttg gaa gat gtt gta cat tat caa ttg ttc tca ttt gat aag Asp Leu Leu Glu Asp Val Val His Tyr Gln Leu Phe Ser Phe Asp Lys 770 775 780	2353
ggt atg atg gac ttg gat aaa aat ggg aga att ttg tcc aga ggt ctt Gly Met Met Asp Leu Asp Lys Asn Gly Arg Ile Leu Ser Arg Gly Leu 785 790 795	2401

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 Ala Asn Ile His His Val Asn Asp Thr Thr Met Val Ile Ser Tyr Leu
 800 805 810 815
 aga ggt ccc aat ctc ttt gtg ttc aac ttt cat cct gtc aat tca tat 2497
 Arg Gly Pro Asn Leu Phe Val Phe Asn Phe His Pro Val Asn Ser Tyr
 820 825 830
 gaa aga tac att ata ggt gtg gaa gaa gct gga gag tat caa gtc aca 2545
 Glu Arg Tyr Ile Ile Gly Val Glu Glu Ala Gly Glu Tyr Gln Val Thr
 835 840 845
 tta aat aca gat gaa aac aag tat ggt ggt aga gga cta ctt ggc cat 2593
 Leu Asn Thr Asp Glu Asn Lys Tyr Gly Gly Arg Gly Leu Leu Gly His
 850 855 860
 gat cag aat att caa aga acc att agt aga aga gct gat gga atg aga 2641
 Asp Gln Asn Ile Gln Arg Thr Ile Ser Arg Arg Ala Asp Gly Met Arg
 865 870 875
 ttt tgc ttg gaa gtg cct ctg cca agt aga agt gct cag gtc tac aag 2689
 Phe Cys Leu Glu Val Pro Leu Pro Ser Arg Ser Ala Gln Val Tyr Lys
 880 885 890 895
 ttg acc cga att cta aga gca tgatcactct agtaatcaaa gtgcctcata 2740
 Leu Thr Arg Ile Leu Arg Ala
 900
 tgatgacaca aaaggaaagg ttctacattg cccttacact gatcaatatt gacacctttc 2800
 cgaggtgagt ttctgtgatt cttgagcaga ctgttggtta gtcaattatc atgaactttt 2860
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 tggcttgta tgggggtcat aagcatccgc cagattaaga tttcacaggc ctcgagtaaa 2980
 accatcactt actttaagga tacacaaaca caccaacggg gtgcaggctc tgataccttc 3040
 taaagtg 3047

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<211> 902

<212> PRT

<213> Solanum tuberosum

<400> 6

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 1 5 10 15

Ser Arg Leu Ser Phe Leu Ser Gln Thr Gly Ser Arg Thr Ser Arg Gln
 20 25 30

Leu Lys Phe Val Arg Ser Arg Arg Ala Arg Val Ser Arg Cys Arg Cys
 35 40 45

Ser Ala Thr Glu Gln Pro Pro Pro Gln Arg Arg Lys Gln Arg Pro Glu
 50 55 60

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Lys Tyr Lys Gln Ser Glu Glu Gly Lys Gly Ile Asp Pro Val Gly Phe
65 70 75 80

Leu Ser Lys Tyr Gly Ile Thr His Lys Ala Phe Ala Gln Phe Leu Arg
85 90 95

Glu Arg Tyr Lys Ser Leu Lys Asp Leu Lys Asp Glu Ile Leu Thr Arg
100 105 110

His Phe Ser Leu Lys Glu Met Ser Thr Gly Tyr Glu Leu Met Gly Met
115 120 125

His Arg Asn Ile Gln His Arg Val Asp Phe Leu Glu Trp Ala Pro Gly
130 135 140

Ala Arg Tyr Cys Ala Leu Ile Gly Asp Phe Asn Gly Trp Ser Thr Thr
145 150 155 160

Gly Asn Cys Ala Arg Glu Gly His Phe Gly His Asp Asp Tyr Gly Tyr
165 170 175

Trp Phe Ile Ile Leu Glu Asp Lys Leu Arg Glu Gly Glu Glu Pro Asp
180 185 190

Lys Leu Tyr Phe Gln Gln Tyr Asn Tyr Ala Glu Asp Tyr Gly Lys Gly
195 200 205

Asp Thr Gly Ile Thr Val Glu Glu Ile Phe Lys Lys Ala Asn Asp Glu
210 215 220

Tyr Trp Glu Pro Gly Glu Asp Arg Phe Ile Lys Ser Arg Tyr Glu Val
225 230 235 240

Ala Ala Lys Leu Tyr Glu Glu Met Phe Gly Pro Asn Gly Pro Gln Thr
245 250 255

Glu Glu Glu Leu Glu Ala Met Pro Asp Ala Ala Thr Arg Tyr Lys Thr
260 265 270

Trp Lys Glu Gln Gln Lys Glu Asp Pro Ala Ser Asn Leu Pro Ser Tyr
275 280 285

Asp Val Val Asp Ser Gly Lys Glu Tyr Asp Ile Tyr Asn Ile Ile Gly
290 295 300

Asp Pro Glu Ser Phe Lys Lys Phe Arg Met Lys Gln Pro Pro Ile Ala
305 310 315 320

Tyr Trp Leu Glu Thr Lys Lys Gly Arg Lys Gly Trp Leu Gln Lys Tyr
325 330 335

Met Pro Ala Leu Pro His Gly Ser Lys Tyr Arg Val Tyr Phe Asn Thr
 340 345 350

Pro Asn Gly Pro Leu Glu Arg Val Pro Ala Trp Ala Asn Phe Val Ile
 355 360 365

Pro Asp Ala Gly Gly Met Ala Leu Ala Val His Trp Glu Pro Pro Pro
 370 375 380

Glu Tyr Ala Tyr Lys Trp Lys His Lys Leu Pro Val Lys Pro Lys Ser
 385 390 395 400

Leu Arg Ile Tyr Glu Cys His Val Gly Ile Ser Gly Gln Glu Pro Lys
 405 410 415

Val Ser Ser Phe Asn Asp Phe Ile Ser Lys Val Leu Pro His Val Lys
 420 425 430

Glu Ala Gly Tyr Asn Ala Ile Gln Ile Ile Gly Val Val Glu His Lys
 435 440 445

Asp Tyr Phe Thr Val Gly Tyr Arg Val Thr Asn Phe Tyr Ala Val Ser
 450 455 460

Ser Arg Tyr Gly Thr Pro Asp Asp Phe Lys Arg Leu Val Asp Glu Ala
 465 470 475 480

His Gly Leu Gly Leu Leu Val Phe Leu Glu Ile Val His Ser Tyr Ala
 485 490 495

Ala Ala Asp Glu Met Val Gly Leu Ser Leu Phe Asp Gly Ala Asn Asp
 500 505 510

Cys Tyr Phe His Thr Gly Lys Arg Gly His His Lys Phe Trp Gly Thr
 515 520 525

Arg Met Phe Lys Tyr Gly Asp Leu Asp Val Leu His Phe Leu Leu Ser
 530 535 540

Asn Leu Asn Trp Trp Val Glu Glu Tyr His Val Asp Gly Phe His Phe
 545 550 555 560

His Ser Leu Ser Ser Met Leu Tyr Thr His Asn Gly Phe Ala Ser Phe
 565 570 575

Thr Gly Asp Met Asp Glu Tyr Cys Asn Gln Tyr Val Asp Lys Glu Ala
 580 585 590

Leu Leu Tyr Leu Ile Leu Ala Asn Glu Val Leu His Ala Leu His Pro
 595 600 605

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Asn Val Ile Thr Ile Ala Glu Asp Ala Thr Leu Tyr Pro Gly Leu Cys
 610 615 620

Asp Pro Thr Ser Gln Gly Gly Leu Gly Phe Asp Tyr Phe Ala Asn Leu
 625 630 635 640

Ser Ala Ser Glu Met Trp Leu Ala Leu Leu Glu Asn Thr Pro Asp His
 645 650 655

Glu Trp Cys Met Ser Lys Ile Val Ser Thr Leu Val Gly Asp Arg Gln
 660 665 670

Asn Thr Asp Lys Met Leu Leu Tyr Ala Glu Asn His Asn Gln Ser Ile
 675 680 685

Ser Gly Gly Arg Ser Phe Ala Glu Ile Leu Ile Gly Asn Ser Leu Gly
 690 695 700

Lys Ser Ser Ile Ser Gln Glu Ser Leu Leu Arg Gly Cys Ser Leu His
 705 710 715 720

Lys Met Ile Arg Leu Ile Thr Ser Thr Ile Gly Gly His Ala Tyr Leu
 725 730 735

Asn Phe Met Gly Asn Glu Phe Gly His Pro Lys Arg Val Glu Phe Pro
 740 745 750

Met Ser Ser Asn Asn Phe Ser Phe Ser Leu Ala Asn Arg Arg Trp Asp
 755 760 765

Leu Leu Glu Asp Val Val His Tyr Gln Leu Phe Ser Phe Asp Lys Gly
 770 775 780

Met Met Asp Leu Asp Lys Asn Gly Arg Ile Leu Ser Arg Gly Leu Ala
 785 790 795 800

Asn Ile His His Val Asn Asp Thr Thr Met Val Ile Ser Tyr Leu Arg
 805 810 815

Gly Pro Asn Leu Phe Val Phe Asn Phe His Pro Val Asn Ser Tyr Glu
 820 825 830

Arg Tyr Ile Ile Gly Val Glu Glu Ala Gly Glu Tyr Gln Val Thr Leu
 835 840 845

Asn Thr Asp Glu Asn Lys Tyr Gly Gly Arg Gly Leu Leu Gly His Asp
 850 855 860

Gln Asn Ile Gln Arg Thr Ile Ser Arg Arg Ala Asp Gly Met Arg Phe
 865 870 875 880

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Cys Leu Glu Val Pro Leu Pro Ser Arg Ser Ala Gln Val Tyr Lys Leu
885 890 895

Thr Arg Ile Leu Arg Ala
900

SwissProt Acc No. or Entry Name	Amino acid No.	SwissProt Acc No. or Entry Name	Amino acid No.
APU_THETU	1251-1331	Q9XED2	101-191
GLGB_SYNY3	22-110	Q08131	137-227
P71095	39-130	GLGB_HUMAN	73-168
Q9RXB0	181-274	Q9V6K7	52-144
PULA_KLEPN	301-395	Q22137	53-147
P70983	1143-1238	Q9RM63	25-149
Q41386	205-298	ISOA_FLASP	36-163
O64454	202-295	ISOA_PSEAY	30-155
O69008	105-191	P73608	22-122
O34587	104-189	O04196	74-177
Q9XDB5	231-319	Q9SPT7	8-110
PULA_THEMA	223-311	Q41742	114-218
Q59319	206-300	GLGX_HAEIN	10-101
YIEL_ECOLI	41-123	Q9RNH5	20-117
Q9RX51	22-100	GLGX_ECOLI	9-104
O66936	24-116	Q9RXP5	13-108
Q59832	141-233	GLGX_MYCTU	24-119
GLGB_STRAU	160-252	Q9X947	18-113
GLGB_BUTFI	24-116	P72691	19-120
GLGB_AGRTU	130-223	P95868	17-117
Q9RQI5	134-226	O84046	11-108
GLGB_ECOLI	122-214	Q9Z8F5	11-108
GLGB_HAEIN	122-214	Q9ZVT2	232-335
GLGB_SYNY3	126-217	Q44528	2-83
GLGB_MYCTU	127-223	Q9X2G0	276-357
Q9RTB7	26-115	Q9X2G0	15-98
GLGB_BACSU	23-115	Q45643	46-114
Q59242	23-115	Q9X2G0	126-217
O84874	117-209	TREZ_ARTSQ	5-90
O49185	62-153	TREZ_MYCTU	2-68
GLGB_YEAST	59-153	Q55088	1-79
Q9Y8H3	47-147	Q53641	1-79

Table 1 Amino acid sequences, contained in the "seed alignment", that are used for producing the HMM for the Pfam isoamylase domain (PF 02922). The table gives the "accession" number (Acc No) or the name (Entry Name), under which the corresponding amino acid sequences are entered in the SwissProt database. Those sections of the amino acid sequences of the corresponding SwissProt entry, which are part of the "seed alignment" (amino acid No.), are also given.

SwissProt Acc No. or Entry Name	Amino acid No.	SwissProt Acc No. or Entry Name	Amino acid No.
AMYM_BACLI	137-479	CDG1_PAEMA	46-426
MALZ_ECOLI	128-522	CDGT_BACOH	44-420
APU_THESA	393-821	AMYB_PAEPO	751-1107
APU_THEET	390-820	AMYA_ASPOR	34-390
CDAS_THEET	136-494	AMY1_DEBOC	49-405
NEPU_BACST	139-497	AMY1_SACFI	40-396
AMYM_BACAD	139-497	AMY1_ECOLI	193-611
AMY2_DICTH	138-470	ISOA_PSEAY	209-652
MALT_AEDAE	29-425	AMY_BUTFI	126-520
MAL2_DROME	30-432	AMY_BACSU	41-383
MAL3_DROME	31-428	AMY_THECU	40-392
MAL1_DROME	35-420	AMY_STRHY	37-360
MAXS_YEAST	17-441	AMY_STRGR	35-372
MAYS_YEAST	22-446	AMY_ALTHA	28-373
MA3S_YEAST	21-443	AMYA_AERHY	26-369
TREC_ECOLI	15-414	AMYC_HUMAN	26-413
TREC_BACSU	16-418	AMYA_DROME	29-396
O16G_BACSP	11-420	AMY1_AERHY	22-379
O16G_BACCE	13-419	AMT4_PSESA	38-387
DEXB_STRMU	13-394	AMY2_ECOLI	12-402
AMY_BACME	44-406	AMY_BACLI	34-420
AMY3_DICTH	39-381	AMY_BACAM	34-422
AMY_STRLI	77-520	AMT6_BACS7	40-426
CDGT_KLEPN	47-463	AMY3_WHEAT	26-348
AMYM_BACST	46-430	AM3A_ORYSA	29-367
CDGT_BACST	47-425	AMYA_VIGMU	24-361
AMYP_BACS8	46-425	AM2A_ORYSA	23-366

Table 2 Amino acid sequences, contained in the "seed alignment", that are used for producing the HMM for the Pfam alpha-amylase domain (PF 00128). The table gives the "accession" number (Acc No) or the name (Entry Name), under which the corresponding amino acid sequences are entered in the SwissProt database. Those sections of the amino acid sequences of the corresponding SwissProt entry, which are part of the "seed alignment" (amino acid No.), are also given.

Table 3 Information for producing the HMM for the Pfam isoamylase domain (PF 02922)

HMMER2.0 [2.3.1]		NAME		isoamylase_N	
ACC		PF02922			
DESC		isoamylase N-term			
LENG		121			
ALPH		Amino			
RF		no			
CS		no			
MAP		yes			
COM		hmmbuild -F HMM_is.ann SEED.ann			
COM		hmmcalibrate --seed 0 HMM_is.ann			
NSEQ		65			
DATE					
CKSUM		3012			
GA		2.3.2.3			
TC		2.3.2.3			
NC		2.1.2.1			
XT		-8455 -4 -1000 -1000 -8455 -4 -8455 -4		-4	
NULT		-4 -8455			
NULE		595 -1558 85 338 -294 453 -1158 197 249 902 -1085 -142 -21 -313 45 531 201 384 -1998 -644			
EVD		-56.839790 0.222419			
HMM		A C D E F G H I K L M N P Q R S T V W Y			
		m->m m->h m->d h->m h->h d->m d->h b->m b->h m->e			
		-32 -5527			
1		433 -2912 -5203 -4583 312 -4575 -3427 -2412 -4218 -2763 739 -4157 2303 -3877 -1058 -777 159 -2330 1852 3373		1	
-		-149 -500 233 43 -381 399 106 -626 210 -466 -720 275 394 45 96 359 117 -369 -294 -249		2	
2		-1 -10660 -11703 -894 -1115 -701 -1378 -32 -1609 373 78 463 -1115 -680 241 -2737 -824 -593 -1619 43 316		2	
-		-503 -4276 -455 1534 635 1339 -2632 -1609 373 78 463 -1115 -680 241 -2737 -824 -593 -1619 43 316		2	
-		-149 -500 233 43 -381 399 106 -626 210 -466 -720 275 394 45 96 359 117 -369 -294 -249		2	
-		-1 -10857 -11899 -894 -1115 -701 -1378 -32 -1609 373 78 463 -1115 -680 241 -2737 -824 -593 -1619 43 316		2	
3		-806 -4386 -2899 -88 -1199 -4001 -313 -1878 1255 -1032 -3488 -2653 2688 -172 105 545 387 -400 -4594 -3938		3	
-		-149 -500 233 43 -381 399 106 -626 210 -466 -720 275 394 45 96 359 117 -369 -294 -249		3	
-		-1 -10916 -11958 -894 -1115 -701 -1378 -32 -1609 373 78 463 -1115 -680 241 -2737 -824 -593 -1619 43 316		3	
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-		-149 -500 233 43 -381 399 106 -626 210 -466 -720 275 394 45 96 359 117 -369 -294 -249		4	
-		-1 -10916 -11958 -894 -1115 -701 -1378 -32 -1609 373 78 463 -1115 -680 241 -2737 -824 -593 -1619 43 316		4	
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-		-149 -500 233 43 -381 399 106 -626 210 -466 -720 275 394 45 96 359 117 -369 -294 -249		5	
-		-1 -10941 -11983 -894 -1115 -701 -1378 -32 -1609 373 78 463 -1115 -680 241 -2737 -824 -593 -1619 43 316		5	
6		2712 446 -5632 -1558 482 -1817 3713 -635 -4593 -29 -2327 -4485 109 -4218 -4397 -260 -3237 343 -3582 161		6	
-		-149 -500 233 43 -381 399 106 -626 210 -466 -720 275 394 45 96 359 117 -369 -294 -249		6	
-		-1 -10941 -11983 -894 -1115 -701 -1378 -32 -1609 373 78 463 -1115 -680 241 -2737 -824 -593 -1619 43 316		6	

Table 3. Sheet 1/9

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10	797	-3873	618	858	-4188	1178	-2048	-3935	-458	-1843	-2963	-2026	1626	-1590	99	164	-514	-1189	683	-15	15
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	16
-	-46	-10244	-5043	-894	-1115	-4637	-59	-1276	467	-1532	-2931	448	230	775	-2097	-2257	-855	-888	-4026	-3345	17
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-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	19
-	-1075	-10201	-931	-894	-1115	-1364	-709	-810	389	-1423	2049	1275	-3064	738	-253	-821	-912	-3067	-3637	-2959	20
12	-847	832	1648	-1300	-3762	-553	1139	-810	389	-1423	2049	1275	-3064	738	-253	-821	-912	-3067	-3637	-2959	21
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	22
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14	-88	1322	-3700	1196	-1379	-398	1869	1265	-2718	-141	1928	-2883	-3139	-2380	-2591	-2162	-1503	1517	-1876	-1529	27
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	28
-	-80	-8931	-4097	-894	-1115	-5563	-31	-2880	499	-2828	-1803	1507	-2408	683	-1068	-1224	-1284	-289	-2998	-2315	29
15	-1344	-2813	2298	288	602	-240	1306	-2880	499	-2828	-1803	1507	-2408	683	-1068	-1224	-1284	-289	-2998	-2315	30
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	31
-	-139	-8846	-3483	-894	-1115	-4086	-88	-4858	-4947	-5141	-4214	-3556	477	-4449	-4699	816	-2415	335	-5331	-5237	32
16	-1947	-2556	-4788	-5046	-5091	3282	-4399	-4858	-4947	-5141	-4214	-3556	477	-4449	-4699	816	-2415	335	-5331	-5237	33
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	34
-	-1391	-8903	-898	-894	-1115	-2384	-307	-2783	864	-2816	-1844	-1122	1166	-728	-1233	-1401	-1440	802	-3046	-2410	35
17	1320	-2772	-1282	2128	-3091	-2427	-1158	-2783	864	-2816	-1844	-1122	1166	-728	-1233	-1401	-1440	802	-3046	-2410	36
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19	500	-3988	418	2	-4310	1492	-2148	-4060	805	-4005	-3078	1770	-1034	395	-585	203	-470	-1409	-4172	-266	42
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	43
-	-32	-10365	-5558	-894	-1115	-138	-3458	-686	627	-4492	-3565	-12	-360	186	-434	81	-490	-4098	-4659	-771	44
20	-804	-4476	-607	-506	-1213	2552	-198	-686	627	-4492	-3565	-12	-360	186	-434	81	-490	-4098	-4659	-771	45
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-	-1	-10817	-11959	-894	-1115	-250	-2654	-686	627	-4492	-3565	-12	-360	186	-434	81	-490	-4098	-4659	-771	47

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21	-903	-3200	-5718	-5083	-433	-1893	-3792	860	-4678	-1338	-2403	-4567	-543	-4301	-4478	-4008	2145	2518	1631	512	21
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22	-1902	-4488	-1380	-132	190	-4097	-528	408	-450	-4488	-3587	1974	-4189	-2312	1656	-1028	1578	714	-4894	444	22
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-	-1	-11023	-12065	-894	-1115	-701	-1378														
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-	-1	-11023	-12065	-894	-1115	-701	-1378														
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-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1	-11023	-12065	-894	-1115	-701	-1378														
27	2849	-4354	-5323	-4910	-5332	-4813	-4712	-4952	-1677	-1991	-4458	-1206	-5320	-4560	-4834	2037	97	-4553	392	-5256	27
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-	-1	-11023	-12065	-894	-1115	-701	-1378														
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-	-1	-11023	-12065	-894	-1115	-701	-1378														
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-	-1	-11023	-12065	-894	-1115	-701	-1378														
34	619	-4558	-156	758	-499	-4076	-481	-1791	587	-2183	-3649	-2714	-4169	-413	962	1507	978	-1017	-4745	910	34
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
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-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1	-11023	-12065	-894	-1115	-701	-1378														

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3 6	557	2801	-1721	-4985	-388	-4905	-248	1189	140	248	-41	-4518	-4956	-1128	-1396	-1302	184	1652	-3666	-218	36
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
3 7	-924	-3659	-6262	-5655	-56	2370	4436	-501	-5277	1969	-2773	-5161	-5523	-4899	-5089	-4605	-1925	945	-4259	-3925	37
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1	-11023	-12065	-894	-1115	-701	-1378	-1027	-2844	-1377	-3222	-282	-198	-1254	-3095	914	-667	-1060	-4386	2201	38
3 8	-3164	-4080	2121	-411	1807	-919	-2937	-1027	-2844	-1377	-3222	-282	-198	-1254	-3095	914	-667	-1060	-4386	2201	38
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3 9	-1317	-4571	1686	-44	3174	-452	570	-4642	414	-4587	-3660	-715	-4166	-2272	-1098	55	-637	-1613	-4755	-4072	39
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4 0	584	-4574	362	369	-4895	-1946	-2733	-4646	367	-1673	-3664	3036	1201	-2273	-1400	-914	-302	-4198	-4758	-4075	40
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-74	-11023	-4329	-894	-1115	-701	-1378	-1027	-2844	-1377	-3222	-282	-198	-1254	-3095	914	-667	-1060	-4386	2201	38
4 1	-1777	-4504	1404	142	-4824	1166	1065	-4574	-2246	-2300	-3593	2273	194	-772	-215	-398	-459	-678	189	96	41
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-	-1080	-10949	-926	-894	-1115	-2265	-337	-3645	-50	-1313	-2663	1007	-267	-1275	-1822	504	735	-3195	-3757	-263	42
4 2	10	-3574	1431	899	-3894	1158	-1734	-3645	-50	-1313	-2663	1007	-267	-1275	-1822	504	735	-3195	-3757	-263	42
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-	-258	-8872	-2622	-894	-1115	-5207	-40	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
4 3	-1897	-3368	980	558	-3688	1508	642	-3438	-1111	-100	-2457	771	-226	1860	-284	-1778	-45	-979	-3552	-2869	43
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
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4 4	-1320	-2790	642	-620	-3110	845	-953	-2859	1750	-2805	-1880	897	64	-494	447	644	269	-338	-2974	-2292	44
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-	-4000	-1761	-638	-49	-4913	-5694	-28	-627	210	-466	-721	275	393	48	95	359	117	-370	-295	-246	
4 5	-1645	-3285	2437	-36	-3659	-1761	-1077	-3545	-1203	-3463	-2733	1862	2482	-734	-1954	-1382	-1715	-3025	-3646	-2736	46
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-	-624	-7357	-1535	-894	-1115	-407	-2026	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
4 6	-2743	-4200	-915	509	-4517	-3717	303	-4263	689	-1027	-3291	-2355	-1213	-385	645	-2625	-805	-1471	5255	-3708	47
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1	-10608	-11650	-894	-1115	-3058	-185	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
4 7	-1155	-4079	2253	-120	-880	-3775	1342	-615	-2051	-2023	-3188	1492	980	383	-2546	-137	-2712	495	-4303	361	48
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4 8	656	-4516	-1114	731	-1260	1230	465	-242	-98	-1569	-3612	-2734	461	159	-654	-1260	819	-242	1382	50	49
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4 9	-3100	-4560	-1116	1388	96	-808	885	-119	-725	-1440	1409	536	-4169	1003	1235	22	807	-488	-4746	-4067	50
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5 0	941	-115	-708	1773	-4860	-1149	-2738	-824	-1301	-2538	698	-1344	-4171	-814	930	554	1279	-254	-4739	-4062	51
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5 1	-420	-3382	-1879	-4044	439	-4712	3032	1305	-703	332	-2575	364	-4775	-722	-67	-3740	41	1148	-3814	285	52
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5 2	-1952	-4573	-58	669	-4895	-4073	-2732	-4645	-493	-4589	-3663	-338	2995	1442	619	-833	-73	-260	-4757	-4074	53
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5 3	-1019	-3213	-1623	-1804	-243	-4921	-3789	-2702	-1610	1632	4259	-4550	-4971	-4279	-4465	-4004	-3320	-593	-3668	798	54
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5 5	-2745	-4145	-2622	504	-415	-3731	392	-4166	1748	-594	-372	-788	1315	-1943	1913	493	-1052	-1625	-4347	183	56
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5 6	-1634	-2867	129	-1035	-3099	918	-1317	-330	201	713	-1982	-1326	-2738	-894	930	1536	714	-2441	-3108	-2486	57
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5 7	-1133	-2513	-524	1978	-2771	1477	-678	-2535	1066	-2508	-1648	-560	-2097	-257	-717	-1002	-1082	-2134	-2676	1915	58
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-	-1253	-7810	-798	-894	-1115	-3061	-184	-	-	-	-	-	-	-	-	-	-	-	-	-	-
5 8	-954	-1426	1440	-1034	-1461	-2223	-963	-1010	-885	-66	1503	-1180	-2298	-782	1512	-1198	1429	886	-1816	-1370	59
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	-
-	-7	-8190	-9232	-894	-1115	-906	-1100	-	-	-	-	-	-	-	-	-	-	-	-	-	-
5 9	-2441	-3911	36	615	-610	-1517	1889	-3980	1236	-227	-3000	1723	366	-1615	1057	-1067	-2380	479	-4095	-3413	60
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	-
-	-78	-10278	-4270	-894	-1115	-1209	-817	-	-	-	-	-	-	-	-	-	-	-	-	-	-
6 0	-272	-4175	1427	-249	-4496	825	-235	-923	391	-577	-3285	978	-3770	-802	1682	165	-1303	-978	-4359	-3876	61
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	-
-	-81	-10580	-4214	-894	-1115	-1882	-456	-	-	-	-	-	-	-	-	-	-	-	-	-	-
6 1	-713	-4275	2377	1673	-4595	133	-2427	-1328	-1103	-4291	-3366	-246	-1321	-1969	-2526	-881	1896	-3897	-4459	-3773	62
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	-
-	-1	-10626	-11668	-894	-1115	-373	-2136	-	-	-	-	-	-	-	-	-	-	-	-	-	-
6 2	-443	-4504	216	-81	1410	1699	-313	-4575	-1074	-4520	-3593	1620	-329	2	-304	636	-837	-4126	-4687	-209	63
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	-
-	-1	-10947	-11990	-894	-1115	-198	-2966	-	-	-	-	-	-	-	-	-	-	-	-	-	-
6 3	-1102	-4838	403	-2956	-707	3185	-502	-4688	-3155	-4786	-746	1388	-4754	-1258	-3682	-3660	-3684	-4391	-4953	421	64
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	-
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Table 3, Sheet 5/9

6 4	-990	-3200	-5718	-5082	406	-4921	-3792	1807	-422	-810	-2403	-1483	-4971	-4300	-4477	-4005	105	2648	1942	674	65
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-	-1	-11023	-12065	-894	-1115	-701	-1378														
6 5	-7684	-6590	-8044	-8406	1262	-7926	-4105	-6567	-7862	-5868	-5867	-6534	-7780	-6676	-7320	-7178	-7532	-6724	6021	1346	66
-	-149	-500	233	43	-381	399	106	-628	210	-466	-720	275	394	45	86	359	117	-369	-294	-249	
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6 6	-1081	-39	-645	2092	-4868	-2001	3120	-4613	-2304	-4563	-3640	-2697	-4153	-2282	-312	1595	958	-1784	-4735	-4055	87
-	-149	-500	233	43	-381	399	106	-628	210	-466	-720	275	394	45	86	359	117	-369	-294	-249	
-	-1	-10999	-12041	-894	-1115	-387	-2088														
6 7	1191	1498	-5739	-5104	-3173	-675	-3816	1715	-4700	1112	-209	-4589	-4992	-4323	-4500	-4028	-68	1675	1543	-3338	68
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6 8	-607	-4400	-3047	467	2483	-4124	-415	-4347	-571	-2213	-3509	-1371	-4215	-707	-22	411	1595	1122	-4629	1250	89
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6 9	-1125	-3258	-5787	-5155	-3223	-430	-3875	1839	-1820	1905	-2463	-4642	-5043	-4379	-4556	-4083	-1271	2065	163	-3395	70
-	-149	-500	233	43	-381	399	106	-628	210	-466	-720	275	394	45	86	359	117	-369	-294	-249	
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7 0	-1005	-4574	94	1232	-1268	-849	305	-4645	-597	-4590	-3663	-423	3130	-2273	-1334	-922	864	-4198	-4757	-4074	71
-	-149	-500	233	43	-381	399	106	-628	210	-466	-720	275	394	45	86	359	117	-369	-294	-249	
-	-799	-11023	-1236	-894	-1115	-701	-1378														
7 1	-1035	-3869	42	-553	-4190	2429	-2028	-3940	383	-1291	-2958	754	531	23	131	-774	-203	-1418	-4052	-3369	72
-	-149	-500	233	43	-381	399	106	-628	210	-466	-720	275	394	45	86	359	117	-369	-294	-249	
-	-1736	-10226	-517	-894	-1115	-3087	-181														
7 2	727	-2766	1622	-596	-3081	-2270	1180	-2828	1228	-563	-1858	1347	-2368	-480	-1030	1120	-1245	-2385	-2953	-2272	73
-	-148	-501	232	48	-382	397	104	-627	211	-467	-722	277	395	47	95	359	118	-368	-286	-250	
-	-3941	-523	-2066	-22	-6038	-5709	-28														
7 3	-2095	-3593	2287	-826	-4113	136	-1685	-3835	-1635	-3872	-3056	2772	865	-1307	-2288	-1905	989	-3409	-4061	-3243	75
-	-149	-500	233	43	-381	399	106	-628	210	-466	-720	275	394	45	86	359	117	-369	-294	-249	
-	-6	-8385	-9427	-894	-1115	-5796	-26														
7 4	-3370	-3802	-3346	-3527	-5498	3620	-3880	-5604	777	-5453	-4841	-3488	-4255	-3494	-3154	-3491	-3683	-4841	-4854	-5028	76
-	-150	-501	234	42	-382	397	104	-627	211	-465	-722	276	393	44	85	363	118	-368	-286	-250	
-	-3549	-131	-9427	-22	-6038	-4725	-56														
7 5	-1261	2000	664	-2358	951	-2717	-1566	-733	-2084	267	-424	-2139	2442	-1824	-2112	228	-1206	633	-1672	-1309	78
-	-149	-500	233	43	-381	399	106	-628	210	-466	-720	275	394	45	86	359	117	-369	-294	-249	
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7 6	892	-4282	1991	467	-4556	495	-2583	504	-1276	-622	-3384	-162	-482	-2140	-2683	-213	284	-489	-4495	-845	79
-	-149	-500	233	43	-381	399	106	-628	210	-466	-720	275	394	45	86	359	117	-369	-294	-249	
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7 7	-874	-3305	-4976	-1454	194	-2338	-3621	1526	-963	1775	-2502	-1534	-110	-1436	-945	-1080	-1758	820	2649	-3384	80
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-	-1	-11023	-12065	-894	-1115	-701	-1378														
7 8	-357	-4572	685	917	-4893	291	1424	-1497	1572	-2482	-3661	-1041	1991	-929	-2819	-681	172	-4194	-4755	-1177	81
-	-149	-500	233	43	-381	399	106	-628	210	-466	-720	275	394	45	86	359	117	-369	-294	-249	
-	-536	-11023	-1691	-894	-1115	-701	-1378														

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7 9	-460	139	903	1067	-4364	1116	2881	-1448	-444	-1437	-3153	877	1180	-1812	-2358	-2514	-2585	-571	-4253	-3580	82
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8 0	-351	-10488	-2216	-894	-1115	-3008	-192	-3887	-556	-1696	-2934	1650	-3471	-1588	-450	-830	-828	-3452	-4032	-3359	83
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8 1	961	-3448	-1830	-230	-3765	-909	654	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	-
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	-
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8 2	-1425	-2189	-1160	-1096	-3294	2933	-1286	-621	209	-466	-720	275	394	45	96	359	120	-370	-295	-250	-
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-	-2273	-761	-2301	-1549	-603	-1681	-539	-3332	-1020	-3281	-2359	198	-2884	490	112	-1882	-253	-2887	-3453	-2771	89
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-	-3	-9452	-10494	-894	-1115	-1361	-711	-2156	-731	530	1415	-3416	-4131	1816	-3398	-1179	229	1180	1903	1485	90
8 4	627	582	-868	-3565	-2609	-4071	385	-2156	-731	530	1415	-3416	-4131	1816	-3398	-1179	229	1180	1903	1485	-
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8 5	-998	-272	-1312	147	944	-4088	-2749	-4547	636	767	-3613	-779	-4180	238	1884	-541	-545	-490	-4716	1812	-
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8 6	-4871	-522	-7273	-6801	-4006	-6725	-5389	401	-6490	-2106	-3511	-6303	-4634	-298	-8337	-5905	-4829	209	-4919	4584	92
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8 7	7	-4545	-2961	83	-4853	1479	-96	-4595	2534	-252	-347	-2720	-4173	-532	-337	-1539	-525	-1911	-4736	5	93
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8 8	-1905	-3714	-6172	-5598	2582	-5424	-3923	389	-837	-1892	-2896	-4990	-5458	-4757	-4969	-4518	-3857	-847	261	4039	94
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8 9	-491	-44	-3807	1600	-142	-4457	-3193	-179	356	-893	-442	-1006	-4533	-1131	2679	-2040	-1632	-273	-4076	53	-
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-	-1	-11023	-12065	-894	-1115	-701	-1378	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	-
9 0	-381	192	-5979	-5354	1663	-5204	-4093	2181	-4980	280	1877	-4850	-5237	-4582	-4765	-4296	-3560	2082	-3938	238	96
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9 1	-1360	856	1256	-178	-448	-4116	2442	-140	738	-1771	-3532	-893	-4207	-601	1	-1669	1115	658	2043	-1166	97
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9 2	-1767	-4492	391	-332	-4797	2082	1139	-650	2283	-2336	-3585	798	-1471	-2241	342	-592	898	872	-4684	-4011	-
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Table 3, Sheet 7/8

9 4	-17	-4552	1435	-686	585	753	1661	-4623	-482	-4568	-3641	1595	-510	-798	-1193	843	-1359	-4174	858	596	100
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9 5	990	-3393	-409	-208	-3713	-2897	1789	-3462	210	-466	-720	275	394	45	96	359	117	-369	-294	-248	
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9 6	-2694	-4027	-1734	21	1263	-3320	986	-4084	-2097	-4097	-3279	170	3097	-1914	-2648	1632	-2688	-3687	-4239	-3490	102
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9 8	763	-3278	2505	1841	-3526	-1860	-998	-3362	-969	-3273	-2473	1657	-2265	-619	-1653	-1329	-1592	-2876	-3450	-2597	104
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9 9	924	1118	-1238	1857	-3128	-2357	-1016	-2870	1001	-799	-1912	420	-2450	1522	180	-1285	-1317	-447	-3010	-2336	122
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10 0	-4244	-5377	-645	-3281	-6758	3521	-4264	-6819	-4334	-6569	-5824	-3558	-5159	-487	-955	-491	-238	-5843	-6723	-5952	123
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-	-4	-9104	-10146	-894	-1115	-4056	-89	-3113	293	-902	-2201	-1368	-2603	825	2944	-213	-1671	-2712	1887	1672	125
10 2	-1738	-3101	318	-1072	-3394	-2715	-1350	-3113	293	-902	-2201	-1368	-2603	825	2944	-213	-1671	-2712	1887	1672	125
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-4	-9260	-10302	-894	-1115	-3745	-112	-2494	187	-2661	-1872	348	-2999	382	-17	-1850	-1768	-164	-3033	1694	126
10 3	-1830	1786	-1979	181	3110	-2914	-1599	-2494	187	-2661	-1872	348	-2999	382	-17	-1850	-1768	-164	-3033	1694	126
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-3	-9439	-10481	-894	-1115	-3895	-100	-1269	489	-3119	-2267	2387	-3039	-1211	-1759	-421	-1882	354	-3396	422	127
10 4	-486	-3147	2145	605	-3366	-2937	-1627	-1269	489	-3119	-2267	2387	-3039	-1211	-1759	-421	-1882	354	-3396	422	127
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-3	-9567	-10609	-894	-1115	-193	-2999	-1170	-1665	-3460	-3460	317	1944	1076	-1285	-804	-1341	651	1747	-760	128
10 5	-1642	-4357	-2912	1666	-1270	-1006	1125	-809	-1170	-1665	-3460	317	1944	1076	-1285	-804	-1341	651	1747	-760	128
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-30	-10913	-5643	-894	-1115	-2658	-249	874	758	-114	-3514	894	-4047	971	-224	68	369	-36	2895	-980	129
10 6	-1173	-4422	150	150	-4731	-3955	-2814	874	758	-114	-3514	894	-4047	971	-224	68	369	-36	2895	-980	129
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-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
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10 8	-3341	-3194	1900	485	588	-4869	-297	-72	-4523	1289	-2395	-4458	-4921	-4178	-1295	-2088	-1548	979	2426	1188	131
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-21	-10996	-6189	-894	-1115	-363	-2168	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	

Table 3, Sheet 8/9

10 9	-117	-4097	-3254	-1038	-4244	-4216	-2903	-119	1662	837	-3236	-2962	385	-851	1231	-865	302	1173	-4396	-3839	132
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11 0	1344	-4030	-1481	-678	-4152	-4269	-2964	1060	-884	1062	-3176	-1173	117	-2623	-546	-280	815	530	-4346	-540	133
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
11 1	-4562	-5414	3954	-4419	-7555	-1661	-5445	-7459	-5967	-7537	-6744	-4536	732	-5224	-6607	436	-1693	-6356	-7702	-7065	134
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
11 2	375	-4583	-3848	-1187	-4813	-4730	-3382	-1424	-2824	-4555	-3786	-3528	3834	-978	62	-3781	-1326	-4174	-4874	-1076	135
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-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
11 4	3042	-4607	-6209	-8125	-6739	540	-5868	200	-6057	-6710	-5828	-1234	-5611	733	-6130	211	-784	-5531	-6964	-6720	137
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
11 5	-1554	-4254	-3118	-2567	1616	-4149	-141	-1803	2314	-2413	-3377	-165	956	-1065	1741	-3071	1002	-1581	-4514	-3916	138
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
11 6	1683	-4540	70	592	1140	57	-2707	-4608	-453	-2223	-3630	225	-4141	-1025	-156	165	-3012	-819	-4725	1981	139
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
11 7	435	976	-5691	-5055	1014	200	-3764	1242	-4650	303	-37	-4539	-4943	-323	-4450	-22	-536	1867	-3630	123	140
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11 8	116	-4535	432	1251	-4851	-355	368	-1120	-2291	-4549	-3626	-417	-308	-474	-2798	928	847	1511	-4721	-101	141
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11 9	89	40	704	-356	-4621	997	-259	-4370	321	-318	-718	-2448	-399	482	-193	844	-1010	1049	-4488	-3807	142
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12 0	-2839	-4311	1556	-525	-4632	-1454	-2471	-4383	-368	-1184	-3401	2127	1394	-2011	2020	-74	-1349	-3933	793	-3812	143
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12 1	-2838	-4293	113	-626	-544	1423	-2474	-4352	-2058	-2372	-3384	22	2430	131	-621	781	-851	451	-4481	-3803	144
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	

Table 3, Sheet 9/9

HMMER
NAME
ACC
DESC
LENG
ALPH
RF
CS
MAP
COM
COM
NSEQ
DATE
CKSUM
GA
TC
NC
XT
MULT
NULE
EVD
HMM

[illegible]

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-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	8
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8	1015	-4092	-2467	1414	-4412	-3593	301	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	10
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9	-798	-3710	1318	381	-4030	-3204	-1867	-3781	-229	-3725	-2800	1805	-3300	-1408	1148	-673	-500	-3332	4434	-3210	13
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10	-754	-3691	95	139	-4012	2378	-1850	-3763	799	-3707	-2780	504	-3285	226	170	-222	-208	-3313	-3874	686	16
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-	-87	-10204	-4120	-894	-1115	-3240	-161	-3520	-1746	-919	-489	-720	275	394	45	96	359	117	-369	-294	21
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-	-166	-10119	-3211	-894	-1115	-3527	-131	-181	276	-1468	-2841	2668	-3381	-463	-2039	-2185	-130	-963	-3940	-3268	30
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-	-224	-8976	-2818	-894	-1115	-4922	-48	-2970	551	-2915	-1990	1351	2468	970	43	-1313	329	-2523	-3081	822	36
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-	-150	-501	237	45	-381	400	105	-627	212	-487	-721	278	393	44	95	358	116	-370	-295	-250	38
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18	-806	-2136	-672	725	-2409	-1787	2069	-2122	-79	-2136	-1251	1334	-1889	-31	-576	1266	1192	187	-2362	-1714	40
-	-149	-500	232	42	-381	398	105	-623	211	-484	-721	275	393	45	97	359	117	-387	-295	-247	41
-	-3106	-442	-2758	-37	-5313	-5259	-38	-2122	-79	-2136	-1251	1334	-1889	-31	-576	1266	1192	187	-2362	-1714	42
19	-1101	-1851	-1203	-809	-1107	-2079	2497	-1776	-717	-1890	-1184	-983	2208	-661	-1099	1211	-1094	-1532	-1558	2020	43
-	-149	-500	233	43	-381	399	106	-626	210	-486	-720	275	394	45	98	359	117	-369	-294	-249	44
-	-10	-7715	-8757	-894	-1115	-3229	-163	-1776	-717	-1890	-1184	-983	2208	-661	-1099	1211	-1094	-1532	-1558	2020	45
20	456	-2091	880	-881	-1511	-2393	-977	-1843	-820	-1991	-1264	-1188	-2490	-787	1184	-1378	-1276	-1631	3621	2048	46
-	-149	-500	233	43	-381	399	106	-626	210	-486	-720	275	394	45	98	359	117	-369	-294	-249	47
-	-7	-8293	-9336	-894	-1115	-1105	-902	-1843	-820	-1991	-1264	-1188	-2490	-787	1184	-1378	-1276	-1631	3621	2048	48
21	-4548	-5007	-4752	-4756	-6164	3702	931	-6680	-3624	-6413	-5801	-4630	-5444	-4302	-411	-4856	-4785	-5961	-5743	-5570	49
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Table 4, Sheet 2/32

22	740	-2742	752	-578	1125	-55	1540	-2808	674	-2756	-1832	332	-2345	-452	691	1244	-1216	-2362	-2927	-2247	24
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-	-148	-501	232	42	-374	397	104	-628	211	-465	-722	276	395	44	95	360	119	-371	-296	-248	
24	-3784	-111	-9662	-19	-8287	-5076	-43	-177	-842	-2307	-1499	-1168	508	-775	-1296	1473	-1252	-226	-2655	-2101	27
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-	-150	-501	235	44	-382	397	104	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
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-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
32	-10	-7741	-8783	-894	-1115	-5295	-37	-2424	-444	-2454	-1592	1798	-2035	-339	-950	-891	1554	-1990	-2686	-2033	
-	1795	-2196	-565	897	-2705	-1787	-749	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	42
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
33	-567	-7741	-1643	-894	-1115	-4278	-76	-2639	-347	-2589	-1721	1280	-1848	2872	-909	-878	-1019	-2187	-2775	-2035	
-	1019	-2549	1220	15	-2866	-1686	-602	-627	213	-466	-721	275	393	45	95	359	117	-370	-295	-244	44
-	-146	-500	232	43	-381	398	105	-627	213	-466	-721	275	393	45	95	359	117	-370	-295	-244	
34	-2649	-255	-8527	-44	-5058	-5334	-38	-2418	-193	-2392	-1509	-373	-1867	-113	1666	1096	-836	-1956	-2579	-1901	
-	-842	-2187	1083	-73	-2670	1600	-538	-626	211	-466	-723	273	388	43	94	357	121	-372	-287	-236	53
-	-151	-502	235	41	-383	403	103	-626	211	-466	-723	273	388	43	94	357	121	-372	-287	-236	
35	-2649	-1232	-1269	-2921	-204	-4299	-75	2029	-1215	-1183	-541	-1214	1812	-1077	-1420	1463	-613	-493	-1794	-1390	
-	-468	-852	-1748	-1375	-1367	-1561	-1139	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	54
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
36	-15	-7122	-8164	-894	-1115	-3735	-113	-2139	1304	-2120	-1225	1410	-1784	86	-407	-828	-674	-1730	3129	-1660	
-	844	-2120	-541	1228	-2414	-1688	-358	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-10	-7701	-8743	-894	-1115	-1988	-416	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	

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37	590	-1848	1080	-1680	-1869	-153	-1528	902	-1529	1445	-1028	-22	-313	-1404	-1840	-451	-1448	-1302	2063	-1818	55
.	-149	-500	233	43	-381	399	108	-628	210	-466	-720	275	394	45	96	359	117	-389	-294	-249	
.	-4	-8953	-8995	-894	-1115	-3914	-99	
38	-1473	-2944	860	-772	-3268	-2446	1829	-3015	1777	-635	-2033	793	-2539	543	1810	54	-183	-2566	-3126	-2445	56
.	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
.	-4	-8047	-10089	-894	-1115	-3200	-166	
39	-1802	-3045	1094	301	197	-2580	1251	-3095	1910	-87	975	38	-2673	-785	-1331	196	912	-2860	-3236	-2561	57
.	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
.	-4	-9230	-10272	-894	-1115	-4772	-54	
40	-360	-4540	-6105	-6279	3176	-5925	-2337	-4407	-18	-3916	-3879	-4657	-5814	-4740	-5283	-5144	-5247	-4497	2202	3735	58
.	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
.	-4	-9230	-10272	-894	-1115	-4772	-54	
41	-2207	3448	-4363	-3804	2865	-3703	2211	-1531	-3416	-289	-1230	-3250	-3744	415	-3228	-2791	58	-1457	1995	950	59
.	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
.	-4	-9230	-10272	-894	-1115	-1292	-757	
42	-2335	1113	-4673	-4038	-357	2872	413	1190	-3835	-2012	-1388	-3528	-3932	-3280	-3439	-2968	-823	489	2158	-2272	60
.	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
.	-2	-9861	-10903	-894	-1115	-802	-1230	
43	-5229	-5553	-6123	-6490	-6106	3663	-6156	-7798	-6977	-7816	-7095	-503	-6308	-6830	-6847	-5444	-5649	-6847	2842	-5752	61
.	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
.	-2	-10248	-11290	-894	-1115	-2023	-408	
44	-2600	-4083	3357	-1838	-4398	-187	346	-4154	-488	-1694	-3178	745	-3841	-108	-2336	-82	-85	-3703	-4266	-3575	62
.	-149	-500	233	43	-381	399	108	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
.	-2	-10288	-11330	-894	-1115	-130	-3539	
45	-7012	-5986	-7498	-7818	1401	-7363	938	-5780	-7378	2298	-817	-6000	-7210	-6118	-6752	-6607	-8866	-5998	4461	1549	63
.	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
.	-1	-10485	-11527	-894	-1115	-701	-1378	
46	-840	-4092	196	-331	-4412	-3593	-2252	-1675	1546	-4107	-3181	1081	-1010	2327	653	-349	-2558	-915	1561	1599	64
.	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
.	-1	-10485	-11527	-894	-1115	-701	-1378	
47	-3634	-5231	826	-129	-757	3120	-3144	-5311	-434	-5236	-4372	905	-4478	-2731	-3537	-788	-1041	-4841	-5412	-4833	65
.	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
.	-1	-10485	-11527	-894	-1115	-701	-1378	
48	-1108	-2725	-5245	-4810	-1161	-4452	-3325	3058	-4207	705	-384	-852	-4500	-3831	-334	-1907	-2841	1482	-3190	-2848	66
.	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
.	-1	-10485	-11527	-894	-1115	-701	-1378	
49	1260	-2803	-1772	-3941	-2771	-1277	-3144	2217	-3884	539	730	-1442	-4369	-3405	-1052	-1332	1925	-2225	-3248	-2886	67
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.	-1	-10485	-11527	-894	-1115	-701	-1378	
50	-597	-4092	1714	1104	-4413	-3593	-2252	-4164	197	-494	-694	1507	-3688	1818	-122	659	-918	-3714	-4276	-3593	68
.	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
.	-1	-10485	-11527	-894	-1115	-701	-1378	
51	-886	-4102	-1336	653	-4423	-1236	1004	-4174	3069	-4117	-3191	545	-3694	291	394	-607	-2587	-3724	-4284	-3602	69
.	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
.	-1	-10485	-11527	-894	-1115	-701	-1378	

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52	78	2795	-428	-4242	-2710	-4369	145	695	-1076	2295	273	-3894	-4423	-49	-3835	-1877	-2804	-2167	866	-2850	70
.	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
53	117	-10485	-11527	-894	-1115	-701	-1378	-1864	-912	-4108	-3181	840	699	-97	-851	-593	40	-714	-4275	-3593	71
.	-150	-502	240	43	-383	401	103	-629	210	-468	-713	275	393	46	95	360	119	-372	-297	-252	
54	-583	-1590	-11527	-327	-2304	-701	-1378	-894	-2540	-1492	-2430	-1139	-4014	-872	-2813	-1575	-171	-1236	-3633	4195	74
.	-2739	-3261	702	-1552	-1049	-1425	-591	-894	-826	210	-466	-720	275	394	45	96	359	117	-369	-294	
.	-149	-500	233	43	-381	399	106	-826	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	75
55	-1	-10485	-11527	-894	-1115	-701	-1378	2398	-7842	2680	-2238	-7944	-7194	-6330	-7081	-7629	-5889	-1773	897	-5384	76
.	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
56	917	-10485	-11527	-894	-1115	-701	-1378	-4164	2745	-4109	-3183	74	-3689	929	-2342	-1598	52	-1108	-4277	-3595	76
.	-149	-500	233	43	-381	399	106	-826	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
57	-1	-10485	-11527	-894	-1115	-701	-1378	-4167	145	-4111	-3184	1061	1224	435	-1051	378	-386	-3717	-4278	-3595	77
.	-680	-4095	1980	794	-4416	741	-2254	-827	211	-467	-721	279	393	44	95	360	118	-370	-295	-250	
58	-150	-501	234	42	-381	399	110	-827	211	-467	-721	279	393	44	95	360	118	-370	-295	-250	
.	-31	-5599	-11527	-2807	-223	-701	-1378	891	225	2098	2191	-1246	-4397	-3501	-3763	-3401	-1516	-2194	863	-2867	88
59	942	-2775	-1042	-4088	-2738	-4341	560	-826	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
.	-149	-500	233	43	-381	399	106	-826	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
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.	-149	-500	233	43	-381	399	106	-826	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
61	-1	-10485	-11527	-894	-1115	-701	-1378	2081	-4267	-2808	-132	-4156	-4557	-3893	-4070	-3598	-472	2155	-3252	2078	88
.	-149	-500	233	43	-381	399	106	-826	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
62	-239	-4233	1152	-2113	-4626	555	-2487	-4376	-694	-4333	-466	1252	-3879	-2038	-2610	-250	2930	-3919	-4510	-3828	89
.	-149	-500	233	43	-381	399	106	-826	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
63	-1	-10485	-11527	-894	-1115	-701	-1378	-2494	-3255	-2818	176	-3423	-4268	-533	-3437	-520	-151	348	-3379	69	90
.	-149	-500	233	43	-381	399	106	-826	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
64	-4777	-4256	-7476	-7167	-4920	-7349	-7445	3081	-7153	141	-3597	-7004	-7060	-7112	-7338	-6742	-170	2423	-6741	-6228	91
.	-149	-500	233	43	-381	399	106	-826	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
65	-1	-10485	-11527	-894	-1115	-701	-1378	-5892	-6008	-1756	-5291	-5711	-7002	1984	-5787	-6378	-6602	-6021	5623	2050	92
.	-149	-500	233	43	-381	399	106	-826	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
66	-5029	-4582	-7496	-6959	122	-7061	-6044	2298	-6715	2037	1608	-6732	-6841	-6001	-6450	-6294	-217	1290	-5182	-5137	93
.	-149	-500	233	43	-381	399	106	-826	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
67	-1	-10485	-11527	-894	-1115	-701	-1378	-3617	-4592	-1531	783	233	1518	-4323	-4625	2681	1511	-3381	-4485	-4145	94
.	-149	-500	233	43	-381	399	106	-826	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
68	-1289	1372	-5290	-4848	-4047	-4330	-4173	-3617	-4592	-1531	783	233	1518	-4323	-4625	2681	1511	-3381	-4485	-4145	
.	-149	-500	233	43	-381	399	106	-826	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
.	-1	-10485	-11527	-894	-1115	-701	-1378	

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87	-1240	-4199	-5920	-8230	-8753	-4440	-5862	-6474	-6122	-8774	-5889	-5051	4130	509	-5883	-3825	-4047	-1240	-8853	-6836	95
-	-149	-5085	-11527	-894	-1115	-701	-1378	-626	210	-466	-720	275	394	45	86	358	117	-369	-294	-249	
88	108	-4065	-7124	-8741	434	-6661	-6322	2424	-6592	-3617	-3454	-6403	2571	-8423	-8620	-5945	-4483	1800	-5951	-5492	96
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89	-1405	-2708	-5187	-4553	2792	-4420	-3289	-775	-4158	-839	-1911	1332	-4470	818	-3988	-303	-28	528	1865	2169	
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-	-188	-9133	-3052	-894	-1115	-4835	-51	-2981	-803	-2964	-2060	2667	-2633	2129	-1307	-1453	323	-183	-3163	-2498	
92	-1792	-1625	-3998	-3375	867	-3348	-2215	1986	893	1010	-718	-2943	-3380	1633	-2846	-2432	-1732	1248	-2099	-1765	100
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-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	86	358	117	-369	-294	-249	
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98	-1625	-4050	-839	-1940	-4352	1882	547	-1615	-803	-1959	-3144	-540	2730	248	-2358	-326	170	-1532	-4245	-3574	108
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	86	358	117	-369	-294	-249	
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99	-1428	-3831	469	208	-4152	596	99	-3903	-325	-1529	1961	1724	-888	1738	-2079	479	-568	-3453	-4014	648	109
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	86	358	117	-369	-294	-249	
-	-1921	-10182	-444	-894	-1115	-3323	-152	-3903	-325	-1529	1961	1724	-888	1738	-2079	479	-568	-3453	-4014	648	
100	372	-2330	-897	-354	-2616	-1985	1916	-2329	2146	-2336	-1448	798	-2082	-215	-725	692	-940	578	-2554	-1910	110
-	-150	-501	239	44	-377	400	104	-626	210	-467	-722	274	398	44	85	359	118	-371	-286	-251	
-	-2157	-369	-9309	-557	-1643	-3400	-144	-2329	2146	-2336	-1448	798	-2082	-215	-725	692	-940	578	-2554	-1910	
81	1078	-2294	1350	-648	300	-485	-800	-2151	-553	-2254	1556	1037	572	-499	-1029	66	-1123	-1846	-2582	1044	114
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	86	358	117	-369	-294	-249	
-	-8	-8597	-8639	-894	-1115	-2783	-225	-2151	-553	-2254	1556	1037	572	-499	-1029	66	-1123	-1846	-2582	1044	

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82	-1461	-2933	894	-749	-3253	-139	1474	-3003	-675	-2949	-2024	1555	-2523	717	848	1813	-1401	-2555	-3117	586	115
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-4	-9004	-10046	-894	-1115	-1884	456	-2923	-1198	-3004	861	669	892	1771	-1680	-1806	1403	888	-3289	1312	116
83	57	-3035	-1842	31	-3246	-482	-1560	-2923	-1198	-3004	861	669	892	1771	-1680	-1806	1403	888	-3289	-294	
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-3	-9540	-10582	-894	-1115	-40	-5194	-4191	-1910	-4148	-3231	-436	-3744	-845	-2419	1681	-2825	-971	3835	-3646	117
84	873	-4137	291	-1124	-4446	1513	-306	-4191	-1910	-4148	-3231	-436	-3744	-845	-2419	1681	-2825	-971	3835	-3646	
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1	-10485	-11527	-894	-1115	-701	-1378	-4659	-4308	-4801	-4205	894	-5163	-3872	-4784	-4205	-1573	-1321	3566	3879	118
85	-4178	-4768	1829	-3445	-3695	-1300	-3742	-4659	-4308	-4801	-4205	894	-5163	-3872	-4784	-4205	-1573	-1321	3566	3879	
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86	-1132	-3799	-861	118	612	-712	4033	-3673	-2003	-1593	1397	819	-3773	-477	-2483	-2604	327	-3356	1886	-377	
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1	-10485	-11527	-894	-1115	-701	-1378	-4135	1128	-1785	-3172	-2248	340	-1811	835	-221	-2571	-1529	-4268	-3583	120
87	-1015	-4079	-928	-1940	-4392	2727	230	-4135	1128	-1785	-3172	-2248	340	-1811	835	-221	-2571	-1529	-4268	-3583	
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1	-10485	-11527	-894	-1115	-701	-1378	-8217	-8274	-7590	-7577	-7492	-7408	-7730	-7762	-7573	-7684	-8017	-5332	4874	121
88	-7416	-6752	-7795	-8171	-4839	-302	-5966	-8217	-8274	-7590	-7577	-7492	-7408	-7730	-7762	-7573	-7684	-8017	-5332	4874	
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-	-1	-10485	-11527	-894	-1115	-701	-1378	-4906	-4122	-4709	233	-4314	-5620	2387	-291	-4803	-4588	-4791	3763	68	122
89	-4666	-5065	3020	-4360	-296	-5588	143	-4906	-4122	-4709	233	-4314	-5620	2387	-291	-4803	-4588	-4791	3763	68	
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1	-10485	-11527	-894	-1115	-701	-1378	-1800	-4177	411	509	-4088	1915	-1144	-3880	-3509	1879	303	1008	-2821	123
90	-285	-2705	-5216	-4581	-2659	-1500	-3296	-1800	-4177	411	509	-4088	1915	-1144	-3880	-3509	1879	303	1008	-2821	
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1	-10485	-11527	-894	-1115	-701	-1378	-761	-549	-1726	-2840	-2438	-3805	801	1137	431	1253	665	-3990	1751	124
91	482	-3709	-2718	364	-791	-3717	285	-761	-549	-1726	-2840	-2438	-3805	801	1137	431	1253	665	-3990	1751	
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1	-10485	-11527	-894	-1115	-701	-1378	-7248	-4767	-7097	-6541	1876	-5333	-3990	-5802	1074	-5057	-6580	-7280	-8167	125
92	-4889	-6628	3602	-2998	-7225	-4711	-4283	-7248	-4767	-7097	-6541	1876	-5333	-3990	-5802	1074	-5057	-6580	-7280	-8167	
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1	-10485	-11527	-894	-1115	-701	-1378	-269	-7412	804	-4944	-6040	-7227	-6136	-6780	-6853	-6877	-5902	2046	4054	126
93	-7029	-5996	-7530	-7846	2273	-7404	-3629	-269	-7412	804	-4944	-6040	-7227	-6136	-6780	-6853	-6877	-5902	2046	4054	
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1	-10485	-11527	-894	-1115	-701	-1378	-4144	1727	-4085	-563	280	-3889	-278	687	-2503	688	-1293	-4268	2168	127
94	-2820	1093	-168	384	987	-129	-2255	-4144	1727	-4085	-563	280	-3889	-278	687	-2503	688	-1293	-4268	2168	
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-21	-10485	-6218	-894	-1115	-701	-1378	-406	1377	7	-3165	586	-3869	1009	-234	493	-1214	-3698	-4259	-3576	128
95	371	-4078	-317	1265	-4397	-1729	212	-406	1377	7	-3165	586	-3869	1009	-234	493	-1214	-3698	-4259	-3576	
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-63	-10466	-4571	-894	-1115	-1141	-872	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
96	-843	191	-1277	-1657	1107	-438	-3165	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-3167	-10404	-172	-894	-1115	-2010	-412	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	

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97	-1053	-2634	1898	158	-2897	-1582	2013	-2698	-340	-2629	-1777	2478	-1882	1472	-923	-857	-1032	-2240	-2803	-2027	130
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-320	-7252	-2377	-894	-1115	-5384	-35	-3343	-1247	-3149	-2741	-1799	-2844	4302	-1383	-2273	-2358	-3074	-2844	-2538	131
98	-2259	-2673	-1597	-1655	-2874	-2426	-1778	-3343	-1247	-3149	-2741	-1799	-2844	4302	-1383	-2273	-2358	-3074	-2844	-2538	
-	-149	-500	233	43	-381	399	105	-627	216	-466	-721	275	393	45	96	359	117	-370	-295	-250	
-	-2113	-387	-7991	-68	-4439	-5394	-35	-4433	-3631	-4384	-3905	-3019	-3114	-3435	-3496	-2545	-2690	-3694	-3457	-3941	133
99	-2307	-2447	-3004	-3307	-4059	-3719	-3189	-4433	-3631	-4384	-3905	-3019	-3114	-3435	-3496	-2545	-2690	-3694	-3457	-3941	
-	-149	-500	233	43	-381	398	105	-627	210	-466	-721	275	393	45	96	360	121	-370	-295	-250	
-	-2113	-387	-7991	-68	-4439	-5394	-35	-4433	-3631	-4384	-3905	-3019	-3114	-3435	-3496	-2545	-2690	-3694	-3457	-3941	133
-	-149	-500	233	43	-381	398	105	-627	210	-466	-721	275	393	45	96	360	121	-370	-295	-250	
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-	-149	-500	233	43	-381	399	108	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-17	-6949	-7991	-894	-1115	-343	-2240	-3903	-1579	-3850	-204	1923	-753	415	106	-2246	-887	-3455	1778	207	136
100	-2365	-3834	2901	-520	-4154	-3339	974	-3903	-1579	-3850	-204	1923	-753	415	106	-2246	-887	-3455	1778	207	
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-2	-10186	-11228	-894	-1115	-84	-3585	-1854	-1854	-4129	-3203	-909	2651	-1812	111	685	1324	-3735	-4297	-399	137
102	-1119	-4113	-534	989	-4433	180	-2271	-4184	-1854	-4129	-3203	-909	2651	-1812	111	685	1324	-3735	-4297	-399	
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1031	-4076	-2475	234	131	-1570	2594	278	1057	-2352	-611	693	-914	1077	1767	-2504	-327	-3694	-4284	-398	138
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-10485	-11527	-894	-1115	-701	-1378	-1378	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
104	-3766	-3535	-5916	-5401	-2942	-840	-3425	-3059	-4991	656	248	-4708	-5245	-4509	-1239	-972	-3702	-2996	1011	3458	139
-	-143	-501	232	42	-382	399	105	-827	212	-467	-721	277	393	44	95	358	116	-370	-295	-245	
-	-42	-5149	-11527	-2670	-247	-701	-1378	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
105	-8252	-7162	-8163	-8550	-8738	3865	-7830	-9779	-8750	-9145	-9067	-8451	-7814	-8612	-8185	-8693	-8516	-9303	-7448	-8752	147
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
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106	-3611	-276	1704	-4311	-6498	-1350	-4820	-6315	-4922	-6428	-5526	2043	-793	-4557	-5305	512	2942	-5291	-8593	-6141	148
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-	-10485	-11527	-894	-1115	-701	-1378	-1378	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
107	-503	-4051	8	1038	-574	-2005	-2265	-1878	1377	260	2254	832	-3697	-1811	1077	-1552	93	-3883	737	-3574	149
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-10485	-11527	-894	-1115	-701	-1378	-1378	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
108	1612	-4106	1904	1843	-4427	-858	-2263	-4178	-659	-4122	-685	-1031	-3697	1321	-2354	-197	-843	-3728	-4289	-3608	150
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-10485	-11527	-894	-1115	-701	-1378	-1378	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
109	11	-4538	3047	1602	-4847	-3855	-2519	-4610	-288	-1877	-3542	-2482	-4021	1329	-2794	-2886	267	-4156	-4718	-4008	151
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-	-10485	-11527	-894	-1115	-701	-1378	-1378	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
110	-2036	1220	-7421	-6835	3516	-6860	-5376	-2914	-6508	2094	660	-6481	-6457	-5667	-6141	-6041	-5012	-3551	403	-4244	152
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-10485	-11527	-894	-1115	-701	-1378	-1378	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
111	-851	-4088	921	828	-349	-3602	-2260	-604	2159	-989	-3179	-2240	-3695	1839	1458	-2510	-2588	-3708	-4273	-3595	153
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
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112	564	-4093	406	1072	-4414	-3593	231	-4165	466	-4109	-3182	1180	-3687	1276	947	1015	780	-3715	-4276	-3593	154
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-284	-249	-
-	-1	-10485	-11527	-894	-1115	-701	-1378	-2909	-7602	2757	3310	-7863	-7137	-6322	-7056	-7412	-5820	-1221	-5316	-5560	155
113	251	-5382	-8381	-7805	-3477	-8030	-6821	-626	210	-466	-720	275	394	45	96	359	117	-369	-284	-249	-
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-284	-249	-
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-	-1	-10485	-11527	-894	-1115	-701	-1378	-4164	1260	-1864	-3181	-565	-3686	-20	1256	-11	240	-709	-4275	-3593	-
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118	-2653	-4128	-124	-729	-778	-1262	4466	-4200	1226	-4143	-3218	354	-3715	446	-370	-1338	-2593	-3750	-4310	-3626	-
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-	-1	-10485	-11527	-894	-1115	-701	-1378	-4166	901	-4110	-462	905	-3687	1166	-743	607	-2560	-3716	-4277	-3594	161
119	1456	-4094	122	1669	-4415	-398	-2253	-4166	901	-4110	-462	905	-3687	1166	-743	607	-2560	-3716	-4277	-3594	-
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120	905	-3975	-3344	-2721	-4151	-4168	-455	-3757	1571	72	-3119	1224	-4233	-2376	2468	-3147	-3042	-301	-4211	1099	-
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-284	-249	-
-	-1	-10485	-11527	-894	-1115	-701	-1378	-7191	-4837	-7077	-6482	1612	-5315	-4063	-5831	-2007	-4937	-6437	-7269	-6213	165
121	-4722	-6205	1052	-3086	-7197	3376	-4350	-7191	-4837	-7077	-6482	1612	-5315	-4063	-5831	-2007	-4937	-6437	-7269	-6213	-
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-284	-249	-
-	-1	-10485	-11527	-894	-1115	-701	-1378	3162	-7240	-1180	3054	-7139	-7098	-6988	-7325	-6879	-4901	1873	-6437	-6132	166
122	-4922	-4389	-7600	-7267	-4589	-7480	-7387	3162	-7240	-1180	3054	-7139	-7098	-6988	-7325	-6879	-4901	1873	-6437	-6132	-
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-284	-249	-
-	-1	-10485	-11527	-894	-1115	-701	-1378	-4190	3130	-1561	-3209	-437	-3717	274	1372	-1594	-2591	-3743	-4287	-879	167
123	362	-4119	-1060	-1952	-4444	-3625	-196	-4190	3130	-1561	-3209	-437	-3717	274	1372	-1594	-2591	-3743	-4287	-879	-
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-284	-249	-
-	-1	-10485	-11527	-894	-1115	-701	-1378	-4190	3130	-1561	-3209	-437	-3717	274	1372	-1594	-2591	-3743	-4287	-879	-
124	-2157	1226	-6830	-6365	-616	-6361	-5646	2243	-6139	479	-3205	-6010	-6258	-5902	-6093	-5571	-1543	2891	-5359	-4952	168
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-284	-249	-
-	-1	-10485	-11527	-894	-1115	-701	-1378	2833	-6544	187	2572	-6548	-6505	-5815	-6253	-6091	-4885	927	-4941	2516	169
125	-4973	-4556	-7390	-6825	-605	-6889	-5739	2833	-6544	187	2572	-6548	-6505	-5815	-6253	-6091	-4885	927	-4941	2516	-
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-284	-249	-
-	-1	-10485	-11527	-894	-1115	-701	-1378	-173	-4190	1545	2374	-4079	-4482	-3812	-3990	-3518	-868	1786	-3169	-178	170
126	790	-2711	-5231	-4595	719	-745	-3305	-173	-4190	1545	2374	-4079	-4482	-3812	-3990	-3518	-868	1786	-3169	-178	-
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-284	-249	-
-	-1	-10485	-11527	-894	-1115	-701	-1378	-	-	-	-	-	-	-	-	-	-	-	-	-	-

Table 4, Sheet 9/32

127	-8466	-7310	4232	-7396	-8700	-7098	-7495	-9750	-8307	-9096	-9042	-7636	-7557	-7951	-8076	-8688	-8607	-9400	-7444	-8581	171
-	-149	-500	233	43	-381	399	106	-628	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1	-10485	-11527	-894	-1115	-701	-1378														
128	1130	-2705	-5224	-4588	2004	-410	-3297	574	-4183	665	-213	-4072	-4476	-3806	-3983	-1769	-1213	2047	-3163	-324	172
-	-149	-500	233	43	-381	399	106	-628	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1	-10485	-11527	-894	-1115	-701	-1378														
129	-202	-4206	-7392	-7072	-4907	-7157	-7171	-452	-7025	-944	-3609	-6853	-6944	-6970	-7177	-6521	-1808	3649	-6601	-6084	173
-	-149	-500	233	43	-381	399	106	-628	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1	-10485	-11527	-894	-1115	-701	-1378														
130	-1570	-2728	-5251	-4616	2039	-4455	-3328	1709	-4212	-885	909	-4101	2203	-3835	-4013	-3541	-400	1465	-3192	427	174
-	-149	-500	233	43	-381	399	106	-628	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1	-10485	-11527	-894	-1115	-701	-1378														
131	-8077	-7138	-7637	-8023	-8516	-7075	-7642	-9858	-8487	-9057	-8951	4459	-7552	-8282	-8070	-8424	-8338	-9174	-7395	-8424	175
-	-149	-500	233	43	-381	399	106	-628	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1	-10485	-11527	-894	-1115	-701	-1378														
132	-8777	-7286	-8125	-8503	-8089	-7246	5476	-9783	-8878	-9076	-9078	-8509	-7683	-8576	-8145	-9272	-8931	-9493	-7256	-7887	176
-	-149	-500	233	43	-381	399	106	-628	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1	-10485	-11527	-894	-1115	-701	-1378														
133	-2889	2001	-4429	-3820	-2867	-4315	-3121	-831	117	-2749	3125	-3660	-4375	-3300	55	996	2538	-2318	-3328	-30	177
-	-149	-500	233	43	-381	399	106	-628	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1	-10485	-11527	-894	-1115	-701	-1378														
134	-82	-10485	-4194	-894	-1115	-701	-1378	-6377	-6284	-6626	96	230	-5088	-5833	-6089	2399	828	-5159	-8787	-6703	178
-	-149	-500	233	43	-381	399	106	-628	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-2	-10404	-11446	-894	-1115	-701	-243	-2687													
135	293	1078	1810	-245	-4380	493	-2259	-4123	-1843	-4081	-3161	-505	954	-1802	-643	621	742	-1825	140	1482	179
-	-149	-500	233	43	-381	399	106	-628	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1	-10485	-11527	-894	-1115	-701	-1378														
136	1323	-4092	1113	1711	450	746	-2252	-4164	-825	-4108	-3181	366	-3686	-7	-903	74	-1029	-1325	-4275	-3593	180
-	-149	-500	233	43	-381	399	106	-628	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1	-10485	-11527	-894	-1115	-701	-1378														
137	-1452	-108	1337	-1115	89	609	3017	-4133	-691	-2342	-3168	437	-3690	385	-2346	1029	-91	-1321	-4263	560	181
-	-149	-500	233	43	-381	399	106	-628	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-2	-10485	-4194	-894	-1115	-701	-1378														
138	1341	-3958	208	1481	-1210	685	-2203	-807	-923	-1650	-3053	-848	1318	-1753	-1129	-287	-899	-799	949	-3493	182
-	-149	-500	233	43	-381	399	106	-628	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
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139	-167	-10404	-3204	-894	-1115	-2010	-412	-3930	216	-3882	-2959	356	-480	-1587	-864	-328	887	-3487	4543	1218	183
-	-149	-500	233	43	-381	399	106	-628	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1	-10485	-11527	-894	-1115	-701	-1378														
140	50	-2754	884	2171	-3064	1269	-892	-2816	-510	-2766	-1855	-805	-2307	-443	864	-1150	-1225	-2372	-2842	750	184
-	-149	-500	233	43	-381	399	106	-628	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1	-10485	-11527	-894	-1115	-701	-1378														
141	-475	-8501	-1848	-894	-1115	-5116	-42	-2815	-428	-2593	2728	1416	-2136	-318	-980	-1014	-1103	-2193	-2795	-2097	185
-	-149	-500	233	43	-381	399	106	-628	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1	-10485	-11527	-894	-1115	-701	-1378														
-	-8	-8034	-8077	-894	-1115	-5240	-39														

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142	-853	-2043	1060	-277	-2257	309	-555	640	1106	-2011	-1164	-564	-1971	1549	-670	-805	-803	1220	-2296	-1886	186
-	-149	-502	232	43	-379	399	103	-629	210	-462	-723	273	391	46	97	359	117	-372	-297	-231	-
-	-3199	-370	-3094	-1784	-495	-825	-1200	-	-	-	-	-	-	-	-	-	-	-	-	-	-
143	491	-2153	235	-3609	3508	-3761	-2613	-133	-3285	-666	-1354	-185	-3816	-2978	-3220	-417	-141	-259	-2606	-2253	185
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	-
-	-2	-9798	-10840	-894	-1115	-1601	-577	-	-	-	-	-	-	-	-	-	-	-	-	-	-
144	-258	-3708	906	-613	-448	-3216	-1875	93	973	-3723	-2798	436	-770	2002	-81	459	-72	225	-3893	21	186
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145	-375	-3789	737	1980	-4108	-251	-1951	-293	784	-3804	-2878	-1928	1280	-1492	1139	-219	-2257	-688	-3973	-3291	197
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	-
-	-2	-10133	-11175	-894	-1115	-1106	-901	-	-	-	-	-	-	-	-	-	-	-	-	-	-
146	480	-2632	527	-3784	-431	222	279	180	-3505	-2487	-1830	-3582	-4203	-3244	-3529	1858	822	1238	-3077	885	198
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	-
-	-2	-10298	-11340	-894	-1115	-135	-3484	-	-	-	-	-	-	-	-	-	-	-	-	-	-
147	66	-3328	-871	-911	814	289	-299	-672	-1401	-140	-2491	1631	-3976	-2359	959	-2853	603	454	215	1373	199
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	-
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148	735	-4092	-1124	486	-4413	652	-236	-4164	1639	-1722	628	-242	-297	265	-727	1141	-898	-1243	-4275	-3593	200
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-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	-
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150	606	-4057	257	-1902	-429	1035	-2233	-1749	1549	-1180	-3148	924	-639	-614	-1007	699	-297	-3676	-4244	763	202
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	-
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-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	-
-	-446	-10459	-1915	-894	-1115	-1265	-776	-	-	-	-	-	-	-	-	-	-	-	-	-	-
152	199	-3692	162	-47	-4013	-384	-1851	-3764	-225	-1337	-2781	2037	1163	852	-174	975	231	-3314	-3875	-3192	204
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	-
-	-105	-10015	-3849	-894	-1115	-3799	-108	-	-	-	-	-	-	-	-	-	-	-	-	-	-
153	-2161	-3339	-2140	-79	588	382	-1859	-3229	631	-389	-110	-1876	1995	979	-841	336	247	-452	-3592	151	205
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	-
-	-1289	-9912	-762	-894	-1115	-4011	-92	-	-	-	-	-	-	-	-	-	-	-	-	-	-
154	356	-1278	-3028	1286	1786	-2793	-1624	727	-2150	-1132	-476	-2208	-2850	-1890	505	-1846	-1269	1038	-1721	1996	206
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	-
-	-135	-8629	-3521	-894	-1115	-5073	-44	-	-	-	-	-	-	-	-	-	-	-	-	-	-
155	414	-1974	2293	-781	775	-2242	-940	-179	-674	-1901	-1123	861	-2327	-605	819	-1181	70	-6	-2286	-1766	207
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	-
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156	-2293	-3722	-466	40	-4025	-3274	-1934	-10	877	-1250	-2816	1348	-3366	104	-2026	135	63	-3334	1226	3252	208
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	-
-	-2	-10089	-11141	-894	-1115	-225	-2793	-	-	-	-	-	-	-	-	-	-	-	-	-	-

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157	71	-4062	527	-350	-4383	1922	-2221	-4134	492	-4078	-3151	-972	457	-11	1582	374	-343	-3584	-4245	-3562	209
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158	-2	-10448	-11490	-894	-1115	-375	-2128	-244	546	-4104	-3178	894	-3687	1057	-2341	-152	-92	-1229	-4273	-3591	210
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-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	-
-	-71	-10485	-4400	-894	-1115	-701	-1378	496	-404	-2566	-1920	-3930	-4423	-3847	-3866	-3446	-1205	-2136	-3651	-249	211
159	-2856	579	-1074	-4338	1305	-253	-623	-828	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	-
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-	-2181	-10377	-361	-894	-1115	-2284	-337	-2402	1092	-2368	-1454	-551	505	-114	1041	-819	-870	-1974	-2552	-1882	214
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163	-3247	-3172	-5235	-4382	-2478	-573	-3019	-722	209	-467	-722	274	392	44	102	358	124	-371	-286	-246	-
-	-150	-501	234	42	-375	397	110	-828	209	-467	-722	274	392	44	102	358	124	-371	-286	-246	-
-	-397	-2618	-3688	-1648	-554	-2653	-250	-3361	932	-1045	-2437	-1571	-720	-1136	1608	-579	-1878	-2946	-3540	-2876	221
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-	-288	-9660	-2475	-894	-1115	-1807	-485	-3551	141	-3486	-2571	-230	2752	890	-1730	-1881	209	-3102	-3663	-2978	222
165	-2004	-3480	1563	403	-76	-2959	1157	-3551	141	-3486	-2571	-230	2752	890	-1730	-1881	209	-3102	-3663	-2978	-
-	-149	-500	233	43	-381	399	106	-626	210	-468	-720	275	394	45	96	359	117	-369	-294	-249	-
-	-3	-9688	-10730	-894	-1115	-3554	-128	735	-200	-3361	-2471	-1673	1374	-1239	-101	-749	-197	-2961	-3580	-2933	223
166	-569	-3357	-1920	-293	-3638	2536	-1680	-626	210	-468	-720	275	394	45	96	359	117	-369	-294	-249	-
-	-149	-500	233	43	-381	399	106	-626	210	-468	-720	275	394	45	96	359	117	-369	-294	-249	-
-	-606	-8729	-1549	-894	-1115	-4287	-75	-367	1980	-2323	-1548	-1474	-2771	-1054	1463	326	-1519	559	2038	396	224
167	-1580	-2399	277	-1234	-82	-690	-1385	-367	1980	-2323	-1548	-1474	-2771	-1054	1463	326	-1519	559	2038	396	-
-	-149	-500	233	43	-381	399	106	-626	210	-468	-720	275	394	45	96	359	117	-369	-294	-249	-
-	-426	-9127	-1978	-894	-1115	-4838	-51	17	295	441	-1144	-1261	-2512	-848	268	-18	-1228	-39	1726	563	225
168	-1289	-1986	496	-1044	-2072	665	2322	-626	210	-468	-720	275	394	45	96	359	117	-369	-294	-249	-
-	-149	-500	233	43	-381	399	106	-626	210	-468	-720	275	394	45	96	359	117	-369	-294	-249	-
-	-285	-8707	-2500	-894	-1115	-5043	-44	-611	-2497	-1644	-1644	1424	-2322	-531	-1111	1631	-1202	-44	-2759	1930	226
169	-1243	-2465	528	-585	-2734	991	-943	-2438	-611	-2497	-1644	1424	-2322	-531	-1111	1631	-1202	-44	-2759	1930	-
-	-149	-500	233	43	-381	399	106	-626	210	-468	-720	275	394	45	96	359	117	-369	-295	-250	-
-	-554	-2243	-3213	-87	-4100	-5139	-42	-2514	-280	-2483	-1575	2156	304	-223	-782	578	-884	-2086	-2670	878	228
170	-1042	-2476	1476	677	476	-1980	-672	-827	210	-467	-721	276	393	44	95	358	116	-370	-295	-250	-
-	-147	-501	234	47	-377	399	105	-827	210	-467	-721	276	393	44	95	358	116	-370	-295	-250	-
-	-1964	-430	-9308	-29	-5634	-2593	-282	708	253	-2806	-1887	385	1812	1242	-1078	-146	735	-2411	-2985	934	230
171	-1350	-2795	-1208	578	-3104	-2328	1428	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	-
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	-
-	-163	-8878	-3259	-894	-1115	-1580	-587	-	-	-	-	-	-	-	-	-	-	-	-	-	-

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172	545	-3282	-343	277	-3501	2235	-1448	-342	-123	-1030	-2372	209	-2882	1554	84	-1696	-1754	-2903	-3467	-2785	231
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-3	-9510	-10552	-894	-1115	-729	-1333	-3893	86	-3838	-2811	2270	-1235	-364	-2070	-54	776	-804	-4005	-3323	232
173	274	-3822	826	-190	-796	1173	-1982	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-2	-10171	-11213	-894	-1115	-804	-1227	-3970	-813	425	-3029	68	1475	-215	510	-1474	182	-1248	-4130	2118	233
174	-2513	1292	212	-864	108	58	-204	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-2	-10357	-11399	-894	-1115	-543	-1673	-3970	-813	425	-3029	68	1475	-215	510	-1474	182	-1248	-4130	2118	233
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
175	-416	-4012	932	231	959	-3576	662	72	-267	-909	-440	-720	275	394	45	96	359	117	-369	-294	234
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-2	-10450	-11492	-894	-1115	-382	-2104	-4163	-668	-4107	-3181	1312	1610	717	-2340	1339	-277	-721	297	-3592	235
176	-1215	-4092	757	28	-512	-1236	1865	-4163	-668	-4107	-3181	1312	1610	717	-2340	1339	-277	-721	297	-3592	235
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1	-10485	-11527	-894	-1115	-701	-1378	-1208	293	-2357	-3180	-74	2452	-319	-161	-313	-2558	-3713	845	-3592	236
177	87	-451	1936	-199	-4411	-955	-2252	-1208	293	-2357	-3180	-74	2452	-319	-161	-313	-2558	-3713	845	-3592	236
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-72	-10485	-4366	-894	-1115	-701	-1378	-2692	-218	-154	-2265	1208	-1550	-985	-2982	856	1868	-2547	481	-4	237
178	-145	1548	-3360	-2786	1809	-439	-2889	-2692	-218	-154	-2265	1208	-1550	-985	-2982	856	1868	-2547	481	-4	237
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-2	-10415	-11457	-894	-1115	-1898	-451	-265	-105	-4039	-3114	2707	94	-696	-349	-2440	-261	-3645	-4209	-203	238
179	-122	1368	1509	-1860	-4342	96	52	-265	-105	-4039	-3114	2707	94	-696	-349	-2440	-261	-3645	-4209	-203	238
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-42	-10415	-5163	-894	-1115	-1898	-451	-1152	677	-745	784	-410	-3922	-2357	-2825	-687	-2582	-2623	4896	1322	239
180	-2642	-3153	-1026	-1101	1324	-1900	32	-1152	677	-745	784	-410	-3922	-2357	-2825	-687	-2582	-2623	4896	1322	239
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-2	-10374	-11416	-894	-1115	-2289	-330	-922	665	-1018	-3062	1359	-3597	-1708	776	-30	-2465	-805	-4160	232	240
181	-2526	290	89	488	-4278	1000	1233	922	665	-1018	-3062	1359	-3597	-1708	776	-30	-2465	-805	-4160	232	240
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-333	-10374	-2283	-894	-1115	-2289	-330	-3778	-220	-3725	-2800	-183	954	-233	-475	1714	-851	-3331	1938	-108	241
182	-486	-3710	307	-1543	1206	240	1404	-3778	-220	-3725	-2800	-183	954	-233	-475	1714	-851	-3331	1938	-108	241
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1263	-10043	-780	-894	-1115	-3733	-113	-1618	374	-113	-1203	1516	-3040	-1614	-2041	-1871	-1668	-1490	2626	1801	242
183	-1728	-2015	-2481	-1929	867	-374	3226	-1618	374	-113	-1203	1516	-3040	-1614	-2041	-1871	-1668	-1490	2626	1801	242
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1036	-8785	-971	-894	-1115	-5012	-45	-2650	2194	-2624	-1910	-1481	-2710	-700	-125	-1793	-1708	-2378	-2606	-2177	243
184	-1792	2872	-2132	-1434	-2813	-2585	3835	-2650	2194	-2624	-1910	-1481	-2710	-700	-125	-1793	-1708	-2378	-2606	-2177	243
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-10	-7758	-8800	-894	-1115	-5292	-37	-451	-2327	-789	-222	-2183	-2704	-1948	-2179	-1740	-1131	1288	-914	-197	244
185	-1177	2374	-3256	-2703	3010	-2639	2355	-451	-2327	-789	-222	-2183	-2704	-1948	-2179	-1740	-1131	1288	-914	-197	244
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-10	-7758	-8800	-894	-1115	-3526	-131	-2701	768	-2643	-1732	1189	818	-288	-889	1444	-1083	-2249	-2813	-2111	245
186	-1135	-2630	1948	-304	-2942	-1997	1333	-2701	768	-2643	-1732	1189	818	-288	-889	1444	-1083	-2249	-2813	-2111	245
-	-150	-501	232	43	-379	402	105	-627	210	-467	-711	274	393	44	95	360	118	-370	-285	-250	
-	-3365	-343	-3129	-29	-5656	-4371	-71	-627	210	-467	-711	274	393	44	95	360	118	-370	-285	-250	

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187	71	-903	-3098	-2485	-875	30	-1413	2394	-2140	-763	-115	-2097	426	-1816	-2039	-1607	316	695	2758	-1021	247
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-8	-8161	-9204	-894	-1115	-774	-1269	405	-184	366	-1824	-270	-3569	-2080	-2529	-255	-721	296	-3039	1888	248
188	-1031	2075	760	69	17	-3494	1783	405	-184	366	-1824	-270	-3569	-2080	-2529	-255	-721	296	-3039	1888	248
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-2	-9900	-10942	-894	-1115	-1667	-545	405	-184	366	-1824	-270	-3569	-2080	-2529	-255	-721	296	-3039	1888	248
189	-2286	1049	-894	-184	2378	629	514	-3744	-593	-1488	-2803	1385	-3360	-360	377	-1247	34	-1479	-2859	-3234	249
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-2	-10090	-11132	-894	-1115	-2048	-399	405	-184	366	-1824	-270	-3569	-2080	-2529	-255	-721	296	-3039	1888	248
190	-1217	811	2503	-2484	-2988	1605	-2438	221	-2347	-2837	-106	-2639	-3773	-2242	775	407	-339	-2411	1221	-2875	250
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-2	-10171	-11214	-894	-1115	-645	-1472	405	-184	366	-1824	-270	-3569	-2080	-2529	-255	-721	296	-3039	1888	248
191	-2536	-3936	168	534	4228	2096	-119	1393	-938	-1731	-3033	462	-896	1150	-2278	-2430	-2475	-1263	881	426	251
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-2	-10381	-11423	-894	-1115	-558	-1640	405	-184	366	-1824	-270	-3569	-2080	-2529	-255	-721	296	-3039	1888	248
192	-675	-4067	-740	-205	-4387	-679	-2227	-4138	-571	-4083	-3156	988	988	447	-2315	1892	1918	-1321	-4250	-413	252
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-2	-10456	-11498	-894	-1115	-414	-2003	405	-184	366	-1824	-270	-3569	-2080	-2529	-255	-721	296	-3039	1888	248
193	947	-4090	1608	-1919	-4410	-1328	-2252	-4160	-472	-2033	1183	1953	-126	1413	877	-571	-1387	-1544	-4274	-3592	253
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1	-10485	-11527	-894	-1115	-701	-1378	405	-184	366	-1824	-270	-3569	-2080	-2529	-255	-721	296	-3039	1888	248
194	-2997	-3142	-128	-3498	1171	-1186	-3014	-2699	-1015	-2999	-2334	-3482	-116	-3116	-337	-3351	-2936	-285	4853	2849	254
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1	-10485	-11527	-894	-1115	-701	-1378	405	-184	366	-1824	-270	-3569	-2080	-2529	-255	-721	296	-3039	1888	248
195	-2619	1393	-46	1043	-654	-353	946	-633	-686	-1611	-3178	1221	-3687	419	-500	1339	1105	-3710	-4273	-674	255
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-61	-10485	-4628	-894	-1115	-701	-1378	405	-184	366	-1824	-270	-3569	-2080	-2529	-255	-721	296	-3039	1888	248
196	-2602	-3745	2499	-2049	-644	-3634	-2309	-3617	-204	-2136	-2868	1352	-3723	-1902	84	-179	22	-1164	2619	2144	256
-	-149	-504	231	40	-371	404	105	-613	215	-470	-725	273	392	43	102	355	115	-373	-289	-247	256
-	-2772	-2761	-502	-2375	-309	-1765	-503	405	-184	366	-1824	-270	-3569	-2080	-2529	-255	-721	296	-3039	1888	248
197	-1540	-2503	1918	-1033	-2697	1705	-1283	-2387	-937	-2524	-1733	-1285	-2656	-925	1509	-1533	-1505	251	3157	-2255	269
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-5	-8661	-9703	-894	-1115	-77	-4268	405	-184	366	-1824	-270	-3569	-2080	-2529	-255	-721	296	-3039	1888	248
198	23	1340	2073	-120	-843	-3569	888	-636	-151	-1214	-3123	1018	-3662	-1774	392	28	501	-3644	-4222	901	270
-	-148	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-2	-10448	-11490	-894	-1115	-375	-2128	405	-184	366	-1824	-270	-3569	-2080	-2529	-255	-721	296	-3039	1888	248
199	-461	-290	619	1891	117	681	-2279	-4015	-1876	-4007	-433	551	-352	-289	-2376	-1119	342	-1236	2947	-768	271
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1	-10485	-11527	-894	-1115	-701	-1378	405	-184	366	-1824	-270	-3569	-2080	-2529	-255	-721	296	-3039	1888	248
200	-715	-4068	669	1304	678	-3599	297	-1256	241	-1157	-458	1822	-3692	787	-979	-1397	537	-1719	1920	-456	272
-	-148	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1	-10485	-11527	-894	-1115	-701	-1378	405	-184	366	-1824	-270	-3569	-2080	-2529	-255	-721	296	-3039	1888	248
201	255	-3362	-3081	-2524	-3437	1545	-2591	-3036	-2404	-2096	-2524	-1211	-915	-494	1309	276	1032	1460	1107	-294	273
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-372	-10485	-2142	-894	-1115	-701	-1378	405	-184	366	-1824	-270	-3569	-2080	-2529	-255	-721	296	-3039	1888	248

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202	-1167	-3767	1430	-92	-4085	1090	-1937	744	-370	-1505	-2857	-799	-3371	2171	-20	-727	-2242	-3387	-2586	-82	274
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
203	-923	-3533	351	1521	-174	-647	604	-3605	-128	-3549	-2822	1793	-3128	1841	-106	-427	903	-3155	-3716	-3033	275
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-756	-9821	-1297	-894	-1115	-2698	-241	-2710	-1086	-624	-1979	399	-2828	-1027	-1580	-103	-1666	-2402	-3095	3340	276
204	-1724	-2850	301	742	1449	-339	-1422	-2710	-1086	-624	-1979	399	-2828	-1027	-1580	-103	-1666	-2402	-3095	3340	276
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-4	-9215	-10257	-894	-1115	-2964	-198	-2723	-4132	-2869	-2368	895	-4637	-3667	-4029	-3714	-3284	-2664	1981	3892	277
205	-468	1610	-19	-4425	2001	-4615	-2413	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-190	-9401	-3038	-894	-1115	-2877	-211	-2113	-3311	2182	-1785	133	-3786	-3050	-3320	-2695	807	-1983	-2837	1349	278
206	-2272	-2368	-3736	-3458	-2327	1779	-2737	-2113	-3311	2182	-1785	133	-3786	-3050	-3320	-2695	807	-1983	-2837	1349	278
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-181	-9392	-3102	-894	-1115	-3606	-124	-3105	-894	-3080	-2170	989	-2735	-852	307	-1551	142	-2684	1764	545	279
207	-379	-3074	896	-979	-3371	378	3695	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-3	-8296	-10338	-894	-1115	-653	-1458	-3538	-280	508	404	-2045	-758	1484	-285	-2285	18	-1520	-3845	1525	280
208	-98	2770	198	-891	-987	-15	429	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-2	-10156	-11198	-894	-1115	-691	-1394	-4043	-1747	-3997	-3075	1162	-3596	-1705	-60	57	-512	-1245	-4172	-3493	281
209	-494	-3983	1162	689	2729	627	-2163	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-2	-10369	-11411	-894	-1115	-655	-1454	-641	-1194	1539	311	-3876	-4392	-1052	-3814	-103	-686	456	1616	1529	282
210	-190	-222	222	-1870	962	-1463	-307	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-2	-10445	-11487	-894	-1115	-1507	-626	-1324	992	-154	-2439	-659	-659	-2344	-2823	-138	-2632	1484	387	833	283
211	643	-3274	580	-1132	981	-423	-2591	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-2	-10445	-11487	-894	-1115	-1507	-626	-4129	639	-4073	757	-564	-3951	16	176	1016	-699	-3679	-4240	-3558	284
212	-19	-4057	510	431	-899	1974	-2216	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-2	-10445	-11487	-894	-1115	-1507	-626	-2497	-4185	2474	2254	-4288	-4853	2186	-4129	-3927	-3287	-2567	-3603	423	285
213	-355	-3235	-5099	-1194	-2927	-4831	-3651	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-2	-10445	-11487	-894	-1115	-358	-2184	-822	-2878	-1755	-2270	-3124	3169	-2744	-1266	-450	-2728	-1518	-3492	-302	286
214	1739	-3082	-182	-3038	-3102	-1439	-2838	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1	-10485	-11527	-894	-1115	-701	-1378	-8772	710	-6721	-6082	256	-5270	-3898	-4984	-4424	-4816	-1142	-6886	-5983	287
215	-4651	464	3855	-3094	-6927	-4683	-4206	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1	-10485	-11527	-894	-1115	-701	-1378	1643	-6862	2782	-2327	-6796	-6720	-5898	-6445	-6466	-5335	-654	967	-980	288
216	-5461	-4988	-7698	-7183	1022	-7248	-5463	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1	-10485	-11527	-894	-1115	-701	-1378														

Table 4, Sheet 15/32

217	-1455	-4071	2159	-1938	-4380	-1778	-2266	-1255	495	-4082	-440	3227	-3699	-1810	-517	-651	-2568	-3687	797	-3587	289
-	-149	-500	233	43	-381	399	106	-628	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
218	-1	-10485	-11527	-894	-1115	-701	-1378	-2256	-4087	-71	-193	-4017	-955	885	-3946	-1878	2462	-2176	3158	2080	
-	-2908	-2760	-5076	-4455	-19	-4433	2308	-2256	-4087	-71	-193	-4017	-955	885	-3946	-1878	2462	-2176	3158	2080	
-	-149	-500	233	43	-381	399	106	-628	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
219	-1	-10485	-11527	-894	-1115	-701	-1378	-2256	-4087	-71	-193	-4017	-955	885	-3946	-1878	2462	-2176	3158	2080	
-	-858	-4092	844	2089	-4413	396	-2251	-1840	-158	-116	-3181	619	-3686	723	545	-490	-536	-3714	-4275	-284	
-	-149	-500	233	43	-381	399	106	-628	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
220	-86	-10485	-4122	-894	-1115	-701	-1378	-4127	-279	-4072	54	3577	-3651	-1757	-653	839	-2528	-3680	-4239	-3559	
-	-2590	432	-492	-968	-4379	-3554	1588	-4127	-279	-4072	54	3577	-3651	-1757	-653	839	-2528	-3680	-4239	-3559	
-	-149	-500	233	43	-381	399	106	-628	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
221	-2	-10400	-11442	-894	-1115	-701	-1378	-4201	-639	-4146	-3220	971	2711	-1826	-2379	-300	1292	-3751	880	-3628	
-	-1507	-4130	30	874	-4450	300	-2284	-4201	-639	-4146	-3220	971	2711	-1826	-2379	-300	1292	-3751	880	-3628	
-	-149	-500	233	43	-381	399	106	-628	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
222	-1	-10485	-11527	-894	-1115	-701	-1378	-4163	92	-2472	-413	-306	-1618	771	-1255	-13	188	257	-4275	1832	
-	260	-4092	726	1607	-4412	-513	-2252	-4163	92	-2472	-413	-306	-1618	771	-1255	-13	188	257	-4275	1832	
-	-147	-502	234	43	-383	397	103	-625	209	-466	-723	280	393	43	93	360	116	-366	-281	-246	
223	-236	-3650	-3805	-2588	-262	-701	-1378	-625	209	-466	-723	280	393	43	93	360	116	-366	-281	-246	
-	-44	1317	-6066	-5505	1402	-5405	-4429	230	-5173	-839	-2606	-5054	-5394	-4849	-5031	-4538	-445	3184	-4243	-3877	
-	-149	-500	233	43	-381	399	106	-628	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
224	-2	-10378	-11420	-894	-1115	-701	-1378	-4213	814	-1463	-2725	460	-3487	-4274	2202	-714	-2751	1420	-3297	1201	
-	65	-2865	-4164	-3574	-2846	-4213	-3013	-4213	814	-1463	-2725	460	-3487	-4274	2202	-714	-2751	1420	-3297	1201	
-	-149	-500	233	43	-381	399	106	-628	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
225	-2	-10450	-11492	-894	-1115	-701	-1378	-4207	1025	-4109	-3182	1775	-3686	1796	695	210	-1255	-3715	-4276	-3593	
-	-651	-4093	1469	319	-4414	-125	-2252	-992	1025	-4109	-3182	1775	-3686	1796	695	210	-1255	-3715	-4276	-3593	
-	-149	-500	233	43	-381	399	106	-628	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
226	-1	-10485	-11527	-894	-1115	-701	-1378	-4162	366	-1668	113	354	-3686	678	408	-2500	-519	-587	-4275	1757	
-	338	-4091	-1137	2053	-4412	-1356	1269	-4162	366	-1668	113	354	-3686	678	408	-2500	-519	-587	-4275	1757	
-	-149	-500	233	43	-381	399	106	-628	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
227	-1	-10485	-11527	-894	-1115	-701	-1378	-4162	366	-1668	113	354	-3686	678	408	-2500	-519	-587	-4275	1757	
-	-1252	-2706	-1848	-4573	971	-4423	-3293	2094	-1151	939	2195	-273	-4473	-626	-3976	-3507	-1544	517	417	1633	
-	-149	-500	233	43	-381	399	106	-628	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
228	-1	-10485	-11527	-894	-1115	-701	-1378	-4162	366	-1668	113	354	-3686	678	408	-2500	-519	-587	-4275	1757	
-	806	-3111	-3504	-1085	-496	-4035	-2787	-228	1468	680	245	-1261	-1626	-1024	-237	-679	-463	149	-3509	2186	
-	-149	-500	233	43	-381	399	106	-628	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
229	-1	-10485	-11527	-894	-1115	-701	-1378	-4162	366	-1668	113	354	-3686	678	408	-2500	-519	-587	-4275	1757	
-	-60	-4091	2196	907	-4411	-1776	-2252	-1262	1126	-996	-3180	1611	-3686	-1792	309	-1480	88	-3713	-4275	-357	
-	-149	-500	233	43	-381	399	106	-628	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
230	-601	-10485	-1557	-894	-1115	-701	-1378	-4162	366	-1668	113	354	-3686	678	408	-2500	-519	-587	-4275	1757	
-	130	-3300	320	1169	473	-864	-1863	-3174	-1511	-3265	-2425	-1883	-3276	-1457	-1991	670	-325	-2858	4062	2148	
-	-147	-501	234	44	-381	398	111	-627	212	-467	-721	275	393	44	95	360	116	-370	-295	-250	
231	-116	-3705	-10929	-1545	-606	-55	-4734	-627	212	-467	-721	275	393	44	95	360	116	-370	-295	-250	
-	880	-2705	-5219	-1393	-487	-146	-3297	1273	-4179	1109	2050	-4070	-4475	-3803	-3981	-319	-958	1575	-3163	-2821	
-	-149	-500	233	43	-381	399	106	-628	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
232	-1	-10485	-11527	-894	-1115	-701	-1378	-4162	366	-1668	113	354	-3686	678	408	-2500	-519	-587	-4275	1757	

Table 4, Sheet 16/32

232	727	-57	-1515	-3685	-2832	-68	-3067	1080	799	359	1459	1063	-4314	-3227	-1673	-82	-1530	871	-3293	-301	316
-	-149	-500	233	43	-381	399	106	-826	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
233	-25	-10485	-5900	-894	-1115	-701	-1378	-4144	1820	-4088	-3161	77	-3665	415	805	-1371	-33	-3694	3083	-3572	317
-	-345	-4072	1466	25	-4393	-131	1146	-828	209	-465	-722	274	395	44	97	358	121	-371	-296	-240	
-	-150	-501	234	42	-382	399	104	-828	209	-465	-722	274	395	44	97	358	121	-371	-296	-240	
-	-40	-5208	-11503	-3012	-191	-446	-1811	-2384	-4390	1748	408	-4253	-4874	-3981	-113	-3721	-3037	-908	-3157	2811	327
234	-3098	557	-5412	-4796	2467	-4633	1098	-2384	-4390	1748	408	-4253	-4874	-3981	-113	-3721	-3037	-908	-3157	2811	327
-	-149	-500	233	43	-381	399	106	-826	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	328
-	-1	-10485	-11527	-894	-1115	-701	-1378	-4144	1820	-4088	-3161	77	-3665	415	805	-1371	-33	-3694	3083	-3572	317
235	-440	-2770	-4991	-4354	-2731	-4413	-3255	134	119	-429	-1971	-3962	-4464	-1018	73	-3489	-1348	621	5347	-2874	328
-	-149	-500	233	43	-381	399	106	-826	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	328
-	-1	-10485	-11527	-894	-1115	-701	-1378	-4144	1820	-4088	-3161	77	-3665	415	805	-1371	-33	-3694	3083	-3572	317
236	518	-2762	-8	-4162	-1014	-233	-3201	1185	-3847	1655	858	446	-4409	-1240	-1731	15	-797	-363	-3212	-256	329
-	-149	-500	233	43	-381	399	106	-826	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	329
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237	-2321	-3792	2018	1012	-4112	4	-1953	-3862	532	-740	381	1728	-3388	-1494	1351	-730	-2260	-3414	841	-3293	330
-	-149	-500	233	43	-381	399	106	-826	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	330
-	-92	-10135	-4037	-894	-1115	-701	-1378	-4144	1820	-4088	-3161	77	-3665	415	805	-1371	-33	-3694	3083	-3572	317
238	-250	-3844	749	681	-4185	569	1082	-3915	1250	-2157	458	-1981	-495	607	655	-2252	491	-3466	1014	1304	331
-	-149	-500	233	43	-381	399	106	-826	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	331
-	-500	-10197	-1775	-894	-1115	-701	-1378	-4144	1820	-4088	-3161	77	-3665	415	805	-1371	-33	-3694	3083	-3572	317
239	-2222	-2815	-28	-2116	41	3002	-2197	-2568	-2074	-2812	-2078	-563	-315	-1959	-2465	200	-2200	-465	1850	-2767	332
-	-149	-500	233	43	-381	399	106	-826	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	332
-	-2227	-8699	-349	-894	-1115	-701	-1378	-4144	1820	-4088	-3161	77	-3665	415	805	-1371	-33	-3694	3083	-3572	317
240	-690	-1030	-1347	667	-1112	1526	-775	-536	-770	-928	2421	-983	-2034	-651	-1069	-950	-658	1348	-1510	-1082	333
-	-149	-500	234	45	-381	398	105	-627	211	-465	-721	276	393	48	98	359	117	-370	-295	-250	333
-	-2848	-650	-2300	-749	-1304	-3702	-115	-627	211	-465	-721	276	393	48	98	359	117	-370	-295	-250	333
241	-1684	-3381	2298	2247	-3628	-1975	-1105	-3463	-1067	-3374	-2571	1228	-2376	-724	-1746	-1436	1284	-2978	-3559	-2700	336
-	-149	-500	233	43	-381	399	106	-826	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	336
-	-265	-7722	-2618	-894	-1115	-701	-1378	-4144	1820	-4088	-3161	77	-3665	415	805	-1371	-33	-3694	3083	-3572	317
242	-498	-1527	-664	-3408	1644	-3248	-2119	1205	-3003	1436	1589	-2893	-3297	-2626	-2804	-2332	-1641	927	2073	992	337
-	-149	-500	233	43	-381	399	106	-826	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	337
-	-4	-8095	-10137	-894	-1115	-701	-1378	-4144	1820	-4088	-3161	77	-3665	415	805	-1371	-33	-3694	3083	-3572	317
243	-241	-4561	1267	-1550	-5048	2895	-2504	-4899	-2538	-4814	-4030	545	-3685	1178	-3239	-874	-3044	-4358	-5001	-4130	338
-	-149	-500	233	43	-381	399	106	-826	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	338
-	-4	-9182	-10224	-894	-1115	-701	-1378	-4144	1820	-4088	-3161	77	-3665	415	805	-1371	-33	-3694	3083	-3572	317
244	707	529	-5359	-4732	472	-4578	76	2402	-4335	-780	262	-4224	-4619	-3983	-4141	-3668	-2843	2418	-3322	-2978	339
-	-149	-500	233	43	-381	399	106	-826	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	339
-	-36	-10450	-5378	-894	-1115	-701	-1378	-4144	1820	-4088	-3161	77	-3665	415	805	-1371	-33	-3694	3083	-3572	317
245	108	-5784	3750	-2898	-6561	-553	-3961	-6451	-304	-8372	-5641	-3250	-5038	-3628	-4889	-171	-4466	-5826	-8560	-844	340
-	-149	-500	233	43	-381	399	106	-826	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	340
-	-2	-10415	-11458	-894	-1115	-701	-1378	-4144	1820	-4088	-3161	77	-3665	415	805	-1371	-33	-3694	3083	-3572	317
246	-882	-4791	-7040	-7394	-6930	3753	-6508	-7307	-7247	-7441	-6597	-5861	-5815	-6771	-6872	-4523	-4737	-6054	933	-6891	341
-	-149	-500	233	43	-381	399	106	-826	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	341
-	-1	-10485	-11527	-894	-1115	-701	-1378	-4144	1820	-4088	-3161	77	-3665	415	805	-1371	-33	-3694	3083	-3572	317

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247	-6543	-5722	-7433	-7597	3802	-7222	-3668	494	-7173	255	-4495	-5988	-7055	-748	-6609	-6447	-6415	-5422	3771	92	342
-	-149	-500	233	43	-381	399	106	-628	210	-486	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1	-10485	-11527	-894	-1115	-701	-1378	-7674	-4419	-7152	33	-6439	-8902	-5393	4226	-6812	-6659	-7468	-6849	-6845	343
248	-6705	-6597	-7597	-6711	-7409	-6618	-5618	-828	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-149	-500	233	43	-381	399	106	-628	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1	-10485	-11527	-894	-1115	-701	-1378	-7674	-4419	-7152	33	-6439	-8902	-5393	4226	-6812	-6659	-7468	-6849	-6845	343
249	-5076	-4650	-7488	-6907	1609	-6991	-5853	2609	-1344	1676	2141	-6665	-6557	-5839	-6306	-6189	-4979	445	-4988	-4973	344
-	-149	-500	233	43	-381	399	106	-628	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1	-10485	-11527	-894	-1115	-701	-1378	-7674	-4419	-7152	33	-6439	-8902	-5393	4226	-6812	-6659	-7468	-6849	-6845	343
250	-7293	-7123	4192	-5805	-7868	-6589	-6618	-8745	-7289	-1940	-8114	-6217	-7106	-6709	-7576	-7234	-7475	-8427	-7251	-7548	345
-	-149	-500	233	43	-381	399	106	-628	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1	-10485	-11527	-894	-1115	-701	-1378	-7674	-4419	-7152	33	-6439	-8902	-5393	4226	-6812	-6659	-7468	-6849	-6845	343
251	2483	-2715	-5223	-4589	961	-4433	154	-752	-4186	-1198	-1919	-4078	-4484	-3812	-3990	-1105	1109	1651	-3176	-2833	346
-	-149	-500	233	43	-381	399	106	-628	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1	-10485	-11527	-894	-1115	-701	-1378	-7674	-4419	-7152	33	-6439	-8902	-5393	4226	-6812	-6659	-7468	-6849	-6845	343
252	2379	-2938	-5404	-2004	-2980	-1281	-3615	714	-4438	-2819	193	-4299	-4697	-4079	-4268	-803	-3050	2448	-3509	-3164	347
-	-149	-500	233	43	-381	399	106	-628	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1	-10485	-11527	-894	-1115	-701	-1378	-7674	-4419	-7152	33	-6439	-8902	-5393	4226	-6812	-6659	-7468	-6849	-6845	343
253	-2633	-4104	-1140	-1930	-4426	-1114	195	-4175	3070	-2035	-3193	1385	362	-1802	351	-251	-866	-3726	-4286	-3605	348
-	-149	-500	233	43	-381	399	106	-628	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1	-10485	-11527	-894	-1115	-701	-1378	-7674	-4419	-7152	33	-6439	-8902	-5393	4226	-6812	-6659	-7468	-6849	-6845	343
254	-2885	-2752	-4977	201	73	530	4521	-2250	-4009	-482	1252	-3962	-4455	-3677	-3896	-1731	-2826	-727	-3185	141	349
-	-149	-500	233	43	-381	399	106	-628	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1	-10485	-11527	-894	-1115	-701	-1378	-7674	-4419	-7152	33	-6439	-8902	-5393	4226	-6812	-6659	-7468	-6849	-6845	343
255	-2968	-2788	-5317	-4683	-582	-1479	-3399	2480	-4281	4	2830	-4171	-988	-3900	-4081	-3612	-2908	1493	-3254	1837	350
-	-149	-500	233	43	-381	399	106	-628	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1	-10485	-11527	-894	-1115	-701	-1378	-7674	-4419	-7152	33	-6439	-8902	-5393	4226	-6812	-6659	-7468	-6849	-6845	343
256	502	-4092	1261	-53	263	-72	-2252	-4183	-186	-4108	-3181	-601	1215	-609	-740	1631	-2558	-3714	1322	641	351
-	-149	-500	233	43	-381	399	106	-628	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1	-10485	-11527	-894	-1115	-701	-1378	-7674	-4419	-7152	33	-6439	-8902	-5393	4226	-6812	-6659	-7468	-6849	-6845	343
257	411	-4077	-106	1023	584	-3597	1678	-1191	1718	-390	8	282	1013	-704	-2346	-1133	-1329	-3696	-4285	-940	352
-	-150	-501	236	43	-379	398	108	-623	209	-488	-722	274	396	44	96	360	116	-366	-296	-251	
-	-5649	-1702	-572	-15	-6554	-701	-1378	-7674	-4419	-7152	33	-6439	-8902	-5393	4226	-6812	-6659	-7468	-6849	-6845	343
258	-411	1839	2192	748	-3114	-2333	-996	-2857	-582	-2816	-1698	-973	1512	1354	242	-1244	-1299	-445	-2995	-2319	354
-	-146	-506	264	43	-375	397	100	-637	184	-479	-736	283	414	28	89	355	113	-372	-288	-222	
-	-2874	-213	-9917	-4062	-89	-4972	-47	-7674	-4419	-7152	33	-6439	-8902	-5393	4226	-6812	-6659	-7468	-6849	-6845	343
259	-1416	-2774	1429	-736	-3035	-2386	1075	242	-666	-2768	-1678	2745	-111	-622	569	-1317	-1357	-2372	-2977	1327	382
-	-149	-500	233	43	-381	399	106	-628	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-5	-8875	-9917	-894	-1115	-701	-1378	-7674	-4419	-7152	33	-6439	-8902	-5393	4226	-6812	-6659	-7468	-6849	-6845	343
260	513	1170	-192	-1660	-2115	2157	-1598	778	-1527	-1967	-1252	1387	-2915	-1416	-1874	-1807	-99	-1536	-2482	897	383
-	-149	-500	233	43	-381	399	106	-628	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-4	-9078	-10121	-894	-1115	-701	-1378	-7674	-4419	-7152	33	-6439	-8902	-5393	4226	-6812	-6659	-7468	-6849	-6845	343
261	557	-4061	-56	474	-4382	1288	-175	-4132	-1802	-2004	-3150	-494	1458	382	-584	756	-301	-3683	796	988	384
-	-149	-500	233	43	-381	399	106	-628	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-2	-10450	-11492	-894	-1115	-701	-1378	-7674	-4419	-7152	33	-6439	-8902	-5393	4226	-6812	-6659	-7468	-6849	-6845	343

Table 4, Sheet 18/32

262	-1153	-2879	1150	-3594	2837	-1439	-292	319	-1519	-1069	-439	-1257	-4293	-3162	1061	-768	-1281	-807	2822	-274	385
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-284	-249	
263	122	-2720	-1621	-4453	-1028	-539	-3269	1036	-4078	1050	-1922	-802	-4456	1084	-3927	-838	-1339	403	3926	595	386
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-284	-249	
-	-1	-10485	-11527	-894	-1115	-701	-1378														
264	-233	-4093	-707	-1918	-4414	-3594	2926	-4165	1889	-4108	-3182	-744	114	1144	1484	-362	548	-1876	-4276	-3593	387
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-284	-249	
265	499	-4092	580	1861	-4413	-1745	-438	708	417	-4108	-3181	205	-1007	934	-2339	753	-672	-258	-4275	-3593	388
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-284	-249	
266	-2891	-2717	-5233	-4599	3037	-4438	-3300	752	-4194	142	283	-889	-4487	-1135	-3994	-1378	-2832	-1132	3346	2415	389
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-284	-249	
267	-503	-3183	-1037	-1492	-3218	-3985	813	306	55	370	2307	-1113	-1033	-2549	1152	-2860	1259	340	884	892	390
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-284	-249	
268	-159	-4092	1289	912	-4413	-955	1047	-4164	313	-4108	-431	-380	-45	1806	-1132	850	248	-1172	-4276	-386	391
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-284	-249	
269	1274	-4093	1238	1709	-4414	-1956	1673	-4165	1186	-4108	-3182	745	-3686	-736	397	-1517	-2558	-1728	-4276	-674	392
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-284	-249	
270	407	-2709	-5213	-4578	-2664	-4428	-3298	1337	-4176	982	2688	-4059	-20	294	-3881	-61	-775	1488	-3168	-2826	393
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-284	-249	
271	85	-4092	262	-1918	-4414	199	975	-4164	1815	-4108	-3182	2049	361	-319	167	-1030	-407	-3714	-4276	1098	394
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-284	-249	
272	1241	-3970	462	1296	-4291	-189	-2129	-4042	-287	-3988	-3059	1684	178	821	69	334	-577	-3592	-4153	-3470	395
-	-284	-10342	-2489	-894	-1115	-2532	-274	-626	210	-466	-720	275	394	45	96	359	117	-369	-284	-249	
273	625	-2676	-1177	670	-171	85	-80	494	232	-329	-1859	-2778	-3779	-2399	-2817	-2704	1049	828	-3084	2108	396
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-284	-249	
274	73	-2503	-1066	-2471	-21	-692	538	-115	1235	-326	890	829	-3575	-2174	-2598	443	794	938	-2908	-180	397
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-284	-249	
275	-80	-2978	1132	1325	1194	-2498	-1158	-3038	794	122	-2069	-1138	-50	-700	870	-265	-98	-2597	-3166	-2487	398
-	-143	-506	231	44	-380	395	104	-626	221	-467	-713	277	393	41	93	358	114	-368	-284	-255	
276	-1944	-436	-10165	-1835	-475	-4841	-51	-366	-1043	-2432	785	-1402	-2734	-980	-1496	1458	735	305	-2800	-2250	410
-	-356	-2494	1117	-163	-2635	1340	-1339	-626	210	-466	-720	275	394	45	96	359	117	-369	-284	-249	
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-284	-249	
-	-4	-9123	-10165	-894	-1115	-2882	-210														

Table 4, Sheet 19/32

277	-1905	-3358	239	-1142	-3665	1869	1510	-3416	-1072	-3364	-2456	-1452	597	1163	1325	-1780	-1846	-2980	-3528	2375	-411	
-	-149	-500	233	43	-381	399	106	-628	210	-466	-720	275	394	45	96	359	117	-369	-294	-249		
278	-3	-9346	-10389	-894	-1115	-972	-1028	-3775	1641	-3719	-2792	-1839	1981	426	570	691	-2169	-3325	-3886	896	412	
-	-1093	-3703	369	430	-4024	-1118	890	-628	210	-466	-720	275	394	45	96	359	117	-369	-294	-249		
-	-149	-500	233	43	-381	399	108	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249		
279	-2	-10028	-11070	-894	-1115	-950	-1052	-3981	326	-3927	-3001	430	1566	-1615	-2163	50	-2380	-1765	2039	-3413	413	
-	-976	-3912	1701	1575	-1111	505	-2074	-3981	326	-3927	-3001	430	1566	-1615	-2163	50	-2380	-1765	2039	-3413	413	
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249		
280	-2	-10276	-11318	-894	-1115	-124	-3599	-4079	893	-4079	448	1507	-4006	129	-3728	692	364	215	1285	-3175	-2830	414
-	429	71	-1863	-1322	834	-1166	-3269	893	-4079	448	1507	-4006	129	-3728	692	364	215	1285	-3175	-2830	414	
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249		
281	-1	-10485	-11527	-894	-1115	-701	-1378	-1048	-4136	-1108	-720	275	394	45	96	359	117	-369	-294	-249		
-	-781	-2711	-348	-807	3229	-4417	185	-1048	-4136	-1108	-720	275	394	45	96	359	117	-369	-294	-249		
-	-149	-500	233	43	-381	399	106	-628	210	-466	-720	275	394	45	96	359	117	-369	-294	-249		
282	-31	-10485	-5610	-894	-1115	-701	-1378	1605	-4155	304	1757	-1446	-4448	-843	-3955	-1828	1924	1040	1341	-208	416	
-	-561	1323	-5196	-4560	109	-4398	-3270	1605	-4155	304	1757	-1446	-4448	-843	-3955	-1828	1924	1040	1341	-208	416	
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249		
283	-2	-10455	-11498	-894	-1115	-412	-2008	290	-1723	239	207	-4162	-4560	-3892	-4072	-3602	-218	2596	-3246	1366	417	
-	-2959	-2779	-5308	-4674	2352	-4516	-3390	290	-1723	239	207	-4162	-4560	-3892	-4072	-3602	-218	2596	-3246	1366	417	
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249		
284	-1	-10485	-11527	-894	-1115	-701	-1378	-6860	-4391	-2189	-6095	-3269	-5218	1419	-5293	-4432	-4888	-6301	-6934	-5886	418	
-	968	-6618	158	-1335	-6920	3180	-4075	-6860	-4391	-2189	-6095	-3269	-5218	1419	-5293	-4432	-4888	-6301	-6934	-5886	418	
-	-149	-500	233	43	-381	399	106	-628	210	-466	-720	275	394	45	96	359	117	-369	-294	-249		
285	-1	-10485	-11527	-894	-1115	-701	-1378	-8036	-5596	-7778	-7325	-1213	-6088	-4906	-8414	-5553	-6009	-7450	-7315	-6874	419	
-	-5864	-7026	-3549	3932	-7732	-5502	-5139	-8036	-5596	-7778	-7325	-1213	-6088	-4906	-8414	-5553	-6009	-7450	-7315	-6874	419	
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249		
286	-1	-10485	-11527	-894	-1115	-701	-1378	1435	-1866	-274	1375	-1502	-862	-3804	-3981	-3509	-1307	2210	2926	1326	420	
-	-242	-2704	-5221	-4585	-167	-4425	101	1435	-1866	-274	1375	-1502	-862	-3804	-3981	-3509	-1307	2210	2926	1326	420	
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249		
287	-1	-10485	-11527	-894	-1115	-701	-1378	1399	-4138	-298	-1913	-4043	-1510	-3772	-750	-532	-2816	-795	4640	1422	421	
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-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249		
288	-1	-10485	-11527	-894	-1115	-701	-1378	-1843	205	-758	-3178	-1104	-3687	1361	-2341	175	-841	-1726	-4273	-915	422	
-	162	-4088	1418	-714	-4408	1367	2467	-1843	205	-758	-3178	-1104	-3687	1361	-2341	175	-841	-1726	-4273	-915	422	
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249		
289	-2847	-10485	-217	-894	-1115	-701	-1378	1572	-1739	-1880	-1160	-1621	-2261	-1561	-1945	1858	1584	1213	-2374	-1999	423	
-	-732	-1200	-2291	-1892	-2006	1184	-1842	1572	-1739	-1880	-1160	-1621	-2261	-1561	-1945	1858	1584	1213	-2374	-1999	423	
-	-148	-503	235	42	-383	402	103	-627	211	-468	-718	278	395	44	93	358	115	-372	-297	-237		
290	-518	-1741	-8690	-3476	-136	-327	-2302	-3928	-1606	-1941	-166	712	-3459	1765	-1027	-635	580	-1514	-4044	-3362	436	
-	588	-3859	1096	-225	-4178	1819	-2025	-3928	-1606	-1941	-166	712	-3459	1765	-1027	-635	580	-1514	-4044	-3362	436	
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249		
291	-86	-10220	-4136	-894	-1115	-3177	-169	-3859	-1553	-1911	-2887	1208	141	-1511	-2060	518	446	-1823	-3983	-3302	437	
-	1059	-3794	1830	-152	-4111	1065	-1969	-3859	-1553	-1911	-2887	1208	141	-1511	-2060	518	446	-1823	-3983	-3302	437	
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249		
-	-2561	-10136	-269	-894	-1115	-3476	-136	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249		

Table 4, Sheet 20/32

282	2610	-1342	-2763	-2844	-3503	678	-2484	-3255	-2594	-3468	-2570	-1940	1729	-2326	-2723	888	-1095	-2280	-3694	-3427	438
-	-149	-500	232	43	-381	401	112	-827	210	-467	-721	277	393	46	95	359	117	-370	-295	-250	
-	-2750	-236	-8628	-41	-5171	-3546	-129	-1496	-753	473	-976	-1123	-2267	-730	2059	773	1741	-1268	-2155	-1683	
283	136	-1631	-1527	-976	-1899	-2091	-1003	-1496	-753	473	-976	-1123	-2267	-730	2059	773	1741	-1268	-2155	-1683	
-	-149	-500	233	43	-381	399	106	-826	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-8	-8080	-9122	-894	-1115	-58	-4437	-4115	-1805	-1498	-531	719	-1394	238	-2311	105	645	-940	-4237	-842	
284	-1186	-4051	1864	-401	-4367	1750	1129	-4115	-1805	-1498	-531	719	-1394	238	-2311	105	645	-940	-4237	-842	
-	-149	-500	233	43	-381	399	106	-826	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-164	-10448	-3225	-894	-1115	-375	-2128	-4027	-957	-1001	-3045	-3	557	-604	-561	575	-12	-3578	-4139	-3456	
285	272	-3956	702	2234	-4277	227	-2115	-4027	-957	-1001	-3045	-3	557	-604	-561	575	-12	-3578	-4139	-3456	
-	-149	-500	233	43	-381	399	106	-826	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-203	-10326	-2940	-894	-1115	-1827	-478	-325	-2390	448	-2058	-2673	610	-2278	25	-2681	-266	512	2653	960	
286	611	-2883	1048	-416	-2916	-1167	1492	-325	-2390	448	-2058	-2673	610	-2278	25	-2681	-266	512	2653	960	
-	-149	-500	233	43	-381	399	106	-826	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-2	-10157	-11199	-894	-1115	-2297	-328	341	149	668	538	-3189	-4017	593	-3185	-416	-86	1089	-3087	43	
287	801	1079	-172	312	-880	-3954	-2752	341	149	668	538	-3189	-4017	593	-3185	-416	-86	1089	-3087	43	
-	-149	-500	233	43	-381	399	106	-826	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-2	-10204	-11246	-894	-1115	-1942	-435	-1582	892	-570	-2987	1038	-689	819	2246	21	-2385	-3520	981	-288	
288	4	-3898	-149	88	-4219	-1463	-2058	-1582	892	-570	-2987	1038	-689	819	2246	21	-2385	-3520	981	-288	
-	-149	-500	233	43	-381	399	106	-826	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-2	-10260	-11303	-894	-1115	-596	-1564	-1186	449	263	-2218	-3006	803	-867	-554	39	187	1072	2048	1040	
289	-1397	-3038	-828	-2801	-504	1085	-2736	-1186	449	263	-2218	-3006	803	-867	-554	39	187	1072	2048	1040	
-	-149	-500	233	43	-381	399	106	-826	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-2	-10415	-11457	-894	-1115	-267	-2567	-1214	-833	294	-283	-727	-137	844	-2813	-3	-2659	548	952	2051	
300	-1177	-3356	1832	-2532	-3429	237	-2595	-1214	-833	294	-283	-727	-137	844	-2813	-3	-2659	548	952	2051	
-	-149	-500	233	43	-381	399	106	-826	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1	-10485	-11527	-894	-1115	-701	-1378	-1463	282	-1404	452	-505	-766	1139	-304	-19	1081	-1324	-4271	-341	
301	1114	-4085	594	798	-654	-1917	-2254	-1463	282	-1404	452	-505	-766	1139	-304	-19	1081	-1324	-4271	-341	
-	-149	-500	233	43	-381	399	106	-826	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-60	-10485	-4636	-894	-1115	-701	-1378	-1235	-116	-4045	-3121	191	76	462	-1170	-203	439	-3650	963	3212	
302	-833	-4031	173	-1079	1188	-1064	-2204	-1235	-116	-4045	-3121	191	76	462	-1170	-203	439	-3650	963	3212	
-	-149	-500	233	43	-381	399	106	-826	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-2	-10426	-11468	-894	-1115	-294	-2438	-318	-1888	-905	-3086	906	728	486	104	-2535	1437	350	-4197	-350	
303	433	-3984	420	767	-1222	-3624	176	-318	-1888	-905	-3086	906	728	486	104	-2535	1437	350	-4197	-350	
-	-149	-500	233	43	-381	399	106	-826	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1	-10485	-11527	-894	-1115	-701	-1378	-649	-1024	-1741	-3145	1134	-3697	-1811	-765	558	-1304	-1729	-4245	852	
304	328	1309	-281	-282	-4353	1769	1890	-649	-1024	-1741	-3145	1134	-3697	-1811	-765	558	-1304	-1729	-4245	852	
-	-149	-500	233	43	-381	399	106	-826	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1	-10485	-11527	-894	-1115	-701	-1378	-1689	82	-1244	-3128	691	-136	-328	962	-2518	133	148	1628	2241	
305	-1216	-4032	-9	-1118	-745	942	-350	-1689	82	-1244	-3128	691	-136	-328	962	-2518	133	148	1628	2241	
-	-149	-500	233	43	-381	399	106	-826	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1	-10485	-11527	-894	-1115	-701	-1378	-3109	-39	-867	1993	942	-900	-829	-2757	458	350	-1139	-3759	1213	
306	-136	-3415	-3012	-2457	1283	719	1555	-3109	-39	-867	1993	942	-900	-829	-2757	458	350	-1139	-3759	1213	
-	-149	-500	233	43	-381	399	106	-826	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1	-10485	-11527	-894	-1115	-701	-1378	-	-	-	-	-	-	-	-	-	-	-	-	-	

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307	819	-4082	1457	1573	-4413	-662	414	-1864	-1832	-2123	-3181	760	-1408	664	-1015	939	267	-3714	-4275	-3593	454
-	-149	-500	233	43	-381	399	106	-628	210	-468	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1	-10485	-11527	-894	-1115	-701	-1378	
308	32	-2705	-5217	-4581	-906	41	-3295	-1012	-4178	1118	251	1098	-4474	-3801	-3979	460	-356	1357	2000	1529	455
-	-149	-500	233	43	-381	399	106	-628	210	-468	-720	275	394	45	96	359	117	-369	-294	-249	
-	-71	-10485	-4400	-894	-1115	-701	-1378	
309	142	-4028	108	874	-4348	-1341	-2192	-1403	-611	-2286	157	1235	1056	1352	-2280	294	1338	-601	-4212	-3531	456
-	-150	-501	234	42	-382	398	105	-627	209	-467	-721	277	393	48	95	360	119	-368	-295	-245	
-	-1126	-2403	-1503	-26	-5804	-267	-2567	
310	-734	-2610	-2963	-495	1059	104	638	-322	-795	-1373	2904	-622	-3585	-2126	-392	916	69	-154	-3006	1234	458
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-2	-9894	-10936	-894	-1115	-3026	-189	
311	-694	-2235	-4645	-4015	-2191	1013	-2798	1221	-3631	1102	1518	-641	-3982	-3272	851	-1354	282	1211	-2692	-2347	459
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-2	-9944	-10986	-894	-1115	-617	-1523	
312	-1055	-2651	-613	-3810	3055	-4167	-3000	-40	-357	532	2046	142	-1479	-3268	-3551	-537	249	-2072	-3086	-75	460
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-2	-10321	-11363	-894	-1115	-149	-3351	
313	-467	-4167	2491	1181	-4487	-185	-2314	-4239	-1905	-4183	-3258	1531	-3743	456	-609	712	63	-3789	-4350	-3663	461
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1	-10485	-11527	-894	-1115	-701	-1378	
314	-1259	-2730	-148	-4808	3644	-4450	-3303	-537	-4204	-55	-1932	-851	-4499	-3826	-4005	-3535	-2845	1077	1010	672	462
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1	-10485	-11527	-894	-1115	-701	-1378	
315	-2622	-4063	394	-68	-350	-1402	503	-985	397	-162	-3155	-2242	1822	-427	553	536	286	-976	-4254	1241	483
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1	-10485	-11527	-894	-1115	-701	-1378	
316	-2746	-3224	1166	-2730	185	347	2505	-2850	-2594	1342	93	441	-4036	-2491	-1349	-1197	-8	-2691	-3603	1960	464
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1	-10485	-11527	-894	-1115	-701	-1378	
317	-203	-3318	-3142	-2584	2102	-381	1857	-1378	-11	-870	526	951	-3981	863	548	-279	-780	-1647	833	1040	465
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1	-10485	-11527	-894	-1115	-701	-1378	
318	216	-4079	1226	-8	883	984	-2256	-1835	141	-1227	-19	-2234	-136	269	384	-215	438	-3697	-4266	568	466
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1	-10485	-11527	-894	-1115	-701	-1378	
319	388	-3951	165	-986	573	-3634	-246	1134	885	-125	-3056	-396	-3725	158	-758	-9	727	662	-4172	-1068	467
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1	-10485	-11527	-894	-1115	-701	-1378	
320	346	551	529	-2498	-181	207	603	1285	-574	1197	-542	-1146	-3947	232	341	-1167	-2655	-2869	-3732	493	468
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1	-10485	-11527	-894	-1115	-701	-1378	
321	-41	-4088	-2468	-4	-4408	111	1186	-1261	400	-2211	-237	732	-883	1891	1097	-102	-291	-1544	-4273	1406	469
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1	-10485	-11527	-894	-1115	-701	-1378	

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322	507	-4092	449	641	-4414	575	44	-4164	1050	-4108	-3181	1550	546	-720	-205	534	-202	-1228	-4276	-3593	470
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-284	-249	
-	-1	-10485	-11527	-894	-1115	-701	-1378	-701	-3946	275	-1944	-363	129	-1121	-3855	20	400	1440	-3195	-283	471
323	1505	-2743	-4902	-1789	1303	-1982	-3231	-70	-3946	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1	-10485	-11527	-894	-1115	-701	-1378	-701	-3946	-466	-720	275	394	45	96	359	117	-369	-294	-249	
324	-1181	-3995	572	-1044	2076	58	605	-1596	57	-562	-3095	-2274	-3713	478	213	1242	-1331	509	-4205	-1010	472
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-961	-10485	-1042	-894	-1115	-701	-1378	-701	-3946	-466	-720	275	394	45	96	359	117	-369	-294	-249	
325	54	-3258	916	-1144	-3561	794	-1470	532	-168	-1378	-2352	55	-2902	791	1381	518	-666	322	-3452	-2781	473
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1288	-9527	-763	-894	-1115	-4529	-64	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
326	-1841	-2600	-1835	-2154	-4644	1586	-2893	-4556	-3135	-4654	-3836	2243	3218	-2885	-3520	-1961	-2222	-3536	-4708	-4269	474
-	-149	-500	232	43	-372	398	105	-627	210	-466	-714	277	393	45	95	359	117	-370	-295	-250	
-	-3410	-1305	-996	-53	-4787	-1602	-576	-626	210	-466	-714	277	393	45	95	359	117	-370	-295	-250	
327	-1431	891	-42	1025	456	1017	-1064	-2967	-846	-2914	-1989	2083	-2498	1034	692	218	-1370	-2520	-3084	-2402	476
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-4	-8991	-10033	-894	-1115	-4118	-86	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
328	-355	-1974	-2372	-1796	2376	-2890	-1625	-1567	1866	-1854	1506	675	-2961	-1491	383	-1881	-1570	1115	-2366	-1940	477
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-4	-9057	-10059	-894	-1115	-2560	-268	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
329	-1797	-2342	-415	287	2146	-1027	-1712	-51	-142	-441	-1509	-1885	-3066	709	-1954	-458	155	-585	3483	743	478
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-3	-9370	-10413	-894	-1115	-925	-1079	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
330	176	-3702	-82	-245	-920	-1338	-1891	146	745	-1033	-231	832	-3324	1918	751	425	-835	-826	-3891	12	479
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-41	-10054	-5194	-894	-1115	-2687	-243	-389	-803	672	921	-883	-3613	-2003	-2483	-296	-51	-1063	773	1369	480
331	-2358	-2946	488	-865	-3010	1948	775	-389	-803	672	921	-883	-3613	-2003	-2483	-296	-51	-1063	773	1369	480
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-2	-10061	-11103	-894	-1115	-1687	-537	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
332	-225	-3817	367	-10	-624	1049	412	-814	1051	-3828	-2808	1912	-3434	-1544	-2091	14	446	5	-4005	-591	481
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-178	-10186	-3115	-894	-1115	-3306	-154	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
333	-2215	-3689	582	-269	-4010	-257	-1848	-3760	469	-56	-2778	781	1787	-206	-283	1184	857	-3311	-3872	-3189	482
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-157	-10010	-3296	-894	-1115	-3810	-107	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
334	-1053	451	-173	368	985	-582	-1891	623	-1580	-3052	-2247	-1944	-988	2031	471	86	-2075	-1017	2776	1210	483
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-2	-9856	-10898	-894	-1115	-3279	-157	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
335	-2120	-3592	1872	-676	-3913	-343	-1752	-3664	159	-823	613	947	-3187	752	658	1133	989	-3214	-3776	-3083	484
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-2547	-9895	-273	-894	-1115	-4043	-90	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
336	-796	-2121	-552	-63	-2376	-1691	-301	-2144	1349	-2097	-1233	2085	-1788	2049	-81	-885	-720	-1755	-2222	1482	485
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-697	-7361	-1408	-894	-1115	-4530	-64	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	

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337	997	-1241	-578	-133	-1517	-1399	-332	-1234	-83	-1405	-619	1518	-1603	-5	-515	1020	-399	-944	-1722	1779	486
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	-
-	-17	-6997	-8039	-894	-1115	-4345	-73	-	-	-	-	-	-	-	-	-	-	-	-	-	-
338	-813	-1193	-2517	-2345	-1917	-1837	-1987	1819	-2146	-1614	-1167	-1892	-2390	-2008	-2230	2830	-1076	-631	-2498	-2045	487
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	-
-	-13	-7341	-8383	-894	-1115	-3330	-151	-	-	-	-	-	-	-	-	-	-	-	-	-	-
339	-927	2366	1639	-228	-2602	-1871	-568	-2325	861	-2315	-1422	-531	-1988	1344	-650	-823	1825	-1917	-2518	-1861	488
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	-
-	-8	-8030	-9072	-894	-1115	-177	-3112	-	-	-	-	-	-	-	-	-	-	-	-	-	-
340	1374	-2592	-5077	-4443	-124	-1761	-3175	-215	-4045	926	3415	-659	-1379	-3873	15	-988	-784	-456	1250	-2707	489
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	-
-	-2	-10357	-11399	-894	-1115	-178	-3103	64	1359	-759	-3164	775	-1426	250	1455	313	-2560	-1811	-4261	1229	490
341	669	-4072	-1127	-1928	-4384	267	-2258	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	-
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	-
-	-1	-10485	-11527	-894	-1115	-701	-1378	-	-	-	-	-	-	-	-	-	-	-	-	-	-
342	-60	-4092	1793	555	-4413	-721	591	-4164	866	-842	-3181	766	-3686	1529	137	-1018	189	-3714	415	58	491
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	-
-	-1	-10485	-11527	-894	-1115	-701	-1378	-	-	-	-	-	-	-	-	-	-	-	-	-	-
343	-2877	521	-228	-4579	1897	-1418	-3294	630	-1972	2065	336	-4067	-1693	-1394	-3978	-1888	-1133	-260	884	733	482
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	-
-	-1	-10485	-11527	-894	-1115	-701	-1378	-	-	-	-	-	-	-	-	-	-	-	-	-	-
344	1114	-3970	600	-1986	-1332	-3628	-2293	-3951	1865	-1722	14	1176	-3720	-798	-921	-102	-163	500	-4186	1177	493
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	-
-	-1	-10485	-11527	-894	-1115	-701	-1378	-	-	-	-	-	-	-	-	-	-	-	-	-	-
345	152	-4092	1011	793	-4413	428	44	-1477	194	-2362	-3181	1659	-3686	1065	-2339	509	905	-2008	-4275	-3593	494
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	-
-	-1	-10485	-11527	-894	-1115	-701	-1378	-	-	-	-	-	-	-	-	-	-	-	-	-	-
346	-218	-2875	-4193	-3609	-142	-1211	-323	115	-123	-219	2818	279	-949	-1143	504	97	-293	-61	2641	338	495
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	-
-	-1	-10485	-11527	-894	-1115	-701	-1378	-	-	-	-	-	-	-	-	-	-	-	-	-	-
347	71	-2705	-5213	-4578	495	657	-3294	1948	-1135	616	1591	-4067	-1693	-3799	-1274	-1209	587	-343	990	565	486
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	-
-	-63	-10485	-4576	-894	-1115	-701	-1378	-	-	-	-	-	-	-	-	-	-	-	-	-	-
348	388	-4039	1017	598	-4360	-547	971	-1236	-306	-1981	871	1250	108	791	-1067	631	842	-3661	-4222	-3539	497
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	-
-	-2	-10423	-11466	-894	-1115	-1793	-491	-	-	-	-	-	-	-	-	-	-	-	-	-	-
349	-1398	-4039	1347	-135	-4360	1020	1623	-1212	777	-371	-3128	55	-3633	489	-321	881	-557	-3661	-4222	379	488
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	-
-	-2	-10423	-11466	-894	-1115	-287	-2470	-	-	-	-	-	-	-	-	-	-	-	-	-	-
350	-2724	-3331	-141	-323	272	-574	-2612	-786	-1221	-688	1421	-1323	-3974	125	-182	-1029	643	802	4091	546	499
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	-
-	-1	-10485	-11527	-894	-1115	-701	-1378	-	-	-	-	-	-	-	-	-	-	-	-	-	-
351	623	-3456	-2964	-82	-57	615	-2532	245	-308	327	533	-572	-3911	2001	-57	-1306	-832	-531	-3791	661	500
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	-
-	-1	-10485	-11527	-894	-1115	-701	-1378	-	-	-	-	-	-	-	-	-	-	-	-	-	-

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352	-156	-4088	25	301	1032	748	486	-4157	319	-991	690	-11	-3687	-39	-1267	1019	341	-3708	258	879	501
-	-149	-500	233	43	-381	399	106	-626	210	-486	-720	275	394	45	96	359	117	-369	-294	-249	
353	-366	-4061	-11527	-894	-1115	-701	-1378	-4108	188	-549	1388	60	-3694	-71	552	426	-337	-783	1504	789	502
-	-149	-500	233	43	-381	399	106	-626	210	-486	-720	275	394	45	96	359	117	-369	-294	-249	
354	-879	-1409	-4984	-1583	-578	-465	1302	-627	-886	449	1708	-3959	1019	-3674	-391	-214	-226	-420	139	2373	503
-	-149	-500	233	43	-381	399	106	-626	210	-486	-720	275	394	45	96	359	117	-369	-294	-249	
355	-1603	-4071	789	-90	-4392	-438	525	-4142	-667	-4087	1182	151	2162	-213	-573	1170	360	-1328	353	-654	504
-	-149	-500	233	43	-381	399	106	-626	210	-486	-720	275	394	45	96	359	117	-369	-294	-249	
356	-78	-10461	-4264	-894	-1115	-1234	-799	-4077	-92	-633	-3095	1912	-795	-688	-2253	633	-2472	-3628	-4189	918	505
-	-149	-500	233	43	-381	399	106	-626	210	-486	-720	275	394	45	96	359	117	-369	-294	-249	
357	-2406	-2237	-739	-24	-5935	-502	-1768	-3138	-838	-3090	-2168	-1232	-210	698	362	-1502	1125	1299	-3264	-2585	507
-	-149	-500	233	43	-381	399	106	-626	210	-486	-720	275	394	45	96	359	117	-369	-294	-249	
358	-285	-2486	-10292	-60	-4624	-1155	-860	-1392	895	-3624	-2699	1357	799	704	-184	-915	153	837	-3794	-3113	509
-	-149	-500	233	43	-381	399	106	-626	210	-486	-720	275	394	45	96	359	117	-369	-294	-249	
359	-1231	884	947	1343	1375	189	-1959	-1477	-501	-939	-2788	-729	-3388	932	-61	-647	-291	-1379	1301	949	510
-	-149	-500	233	43	-381	399	106	-626	210	-486	-720	275	394	45	96	359	117	-369	-294	-249	
360	-422	-4082	-177	-744	-4399	-3596	812	-1474	1870	-1007	-3172	1163	-3689	-635	940	-409	-349	259	3343	-879	511
-	-149	-500	233	43	-381	399	106	-626	210	-486	-720	275	394	45	96	359	117	-369	-294	-249	
361	2063	-3835	-284	-2073	-4049	-3672	-2345	-3729	-1880	256	1615	1147	-3762	1155	-721	539	-297	-1175	-4086	-3475	512
-	-149	-500	233	43	-381	399	106	-626	210	-486	-720	275	394	45	96	359	117	-369	-294	-249	
362	-83	-2706	-5208	-4573	1133	57	-3293	500	-4171	-12	480	508	-4473	-3797	-1508	-885	358	2404	-3163	-2821	513
-	-149	-500	233	43	-381	399	106	-626	210	-486	-720	275	394	45	96	359	117	-369	-294	-249	
363	-2922	-2751	-5249	-4619	-2714	-4471	-3353	366	-4221	-66	-1957	1891	-4523	-3850	-4031	-463	2587	1278	2337	-2861	514
-	-149	-500	233	43	-381	399	106	-626	210	-486	-720	275	394	45	96	359	117	-369	-294	-249	
364	-6591	-5749	-7397	-7594	3911	-7189	-3596	-5428	-7161	426	-4871	-5931	-7055	-729	-6595	-6411	-8467	69	2012	1759	515
-	-149	-500	233	43	-381	399	106	-626	210	-486	-720	275	394	45	96	359	117	-369	-294	-249	
365	-1398	-3732	-6399	-5783	-175	-5697	-4594	1828	-5425	1541	186	-5350	-5603	-4940	-5204	-4820	-3937	2430	2295	-3993	516
-	-149	-500	233	43	-381	399	106	-626	210	-486	-720	275	394	45	96	359	117	-369	-294	-249	
366	-1199	728	2819	1540	-4376	1163	-2266	-1180	-1852	-4079	-3161	-230	-3698	-1810	-809	-1034	-1084	-1474	-4260	-3585	517
-	-149	-500	233	43	-381	399	106	-626	210	-486	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1	-10485	-11527	-894	-1115	-701	-1378	-4108	188	-549	1388	60	-3694	-71	552	426	-337	-783	1504	789	

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367	-3525	-4145	-6117	-6472	-6811	-4397	-6004	-6617	-6593	-6893	-5938	3991	-5207	-6045	-6340	1494	-990	-1177	-7031	-6952	518
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
368	-8351	-7039	-8010	-8359	-4914	-7245	5446	-8380	-8236	-7682	-7739	-7788	-7602	-7853	-7738	-8455	-8411	-8363	437	-4466	519
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1	-10485	-11527	-894	-1115	-701	-1378	-7880	-5377	-7635	-7175	-4028	-5899	-4617	-6337	-5333	-5630	-7322	-7358	-6716	520
369	-5713	-7209	4171	-1139	-7691	-5309	-4876	-7880	-5377	-7635	-7175	-4028	-5899	-4617	-6337	-5333	-5630	-7322	-7358	-6716	520
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1	-10485	-11527	-894	-1115	-701	-1378	-7880	-5377	-7635	-7175	-4028	-5899	-4617	-6337	-5333	-5630	-7322	-7358	-6716	520
370	-2724	-3336	-3119	-2562	-3404	-1240	-2610	-841	-2438	-1922	2315	1570	-1231	2033	-868	-637	2484	-1128	-3694	-3212	521
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-36	-10485	-5377	-894	-1115	-701	-1378	-7880	-5377	-7635	-7175	-4028	-5899	-4617	-6337	-5333	-5630	-7322	-7358	-6716	520
371	-192	-4062	-600	735	-4383	533	-2221	-4133	-171	-4078	1177	830	1627	1762	-823	84	-2528	-849	-4245	550	522
-	-125	-10450	-3599	-894	-1115	-1420	-675	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
372	-1141	-3709	-4623	-4041	-4378	-4271	-3670	-3967	-3223	-4210	265	-3864	529	-3488	3785	-1709	105	-3678	-4619	-118	523
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1658	-10326	-551	-894	-1115	-2638	-253	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
373	82	-2585	-1301	254	-2969	1681	-1268	1213	-960	-2739	-1898	2254	-2584	-871	-1448	403	-1457	-2290	-3024	-2414	524
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1076	-2568	-1486	-91	-4030	-5056	-44	-2796	-450	-2756	-1901	-755	-2306	1644	-881	-1230	1816	-2389	-2927	-2269	526
374	-1367	-2757	-684	762	-3061	-2109	3698	-2796	-450	-2756	-1901	-755	-2306	1644	-881	-1230	1816	-2389	-2927	-2269	526
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-8	-8039	-8081	-894	-1115	-4127	-85	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
375	1394	-1810	-3140	-2842	1387	2255	-2607	-2887	-2712	-3150	-2360	-2340	1262	-2491	-2885	894	-1555	-2316	-3527	-3183	527
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-7	-8232	-8274	-894	-1115	-3538	-130	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
376	849	-1609	-3510	-3089	-1549	1636	-2112	-1290	-2796	2090	-970	-2625	-3110	-2498	-2731	-2012	-1618	-1193	-2101	1259	528
-	-150	-501	232	44	-382	401	105	-627	214	-467	-721	274	393	48	97	358	116	-370	-295	-250	
-	-1693	-536	-9575	-26	-5789	-2879	-211	-627	214	-467	-721	274	393	48	97	358	116	-370	-295	-250	
377	-226	-3139	1871	1010	-3451	1305	-1240	-3212	-871	-3152	-2238	1334	134	921	-1397	81	-1585	-2757	-3321	-2616	530
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-4	-8935	-8977	-894	-1115	-86	-4118	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
378	-809	-2678	397	-4494	2346	529	-3251	1288	-4103	-791	89	-897	-4434	-3738	-3925	880	-2783	1385	-3135	-2791	531
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-2	-10447	-11489	-894	-1115	-369	-2148	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
379	562	-3668	-462	-775	-69	-236	-422	-464	-709	1303	473	-855	-1549	127	-937	83	468	-107	-4111	-249	532
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1	-10485	-11527	-894	-1115	-701	-1378	-7880	-5377	-7635	-7175	-4028	-5899	-4617	-6337	-5333	-5630	-7322	-7358	-6716	520
380	-743	-3979	-1125	-82	-111	-3625	-2289	-874	-1891	-3974	-3082	-613	-987	1020	-679	1753	2083	394	850	-3542	533
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1	-10485	-11527	-894	-1115	-701	-1378	-7880	-5377	-7635	-7175	-4028	-5899	-4617	-6337	-5333	-5630	-7322	-7358	-6716	520
381	-862	658	-514	224	10	-4134	1018	-475	-3061	495	-333	-3271	-4202	431	2132	-150	-868	738	-3403	395	534
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1	-10485	-11527	-894	-1115	-701	-1378	-7880	-5377	-7635	-7175	-4028	-5899	-4617	-6337	-5333	-5630	-7322	-7358	-6716	520

Table 4, Sheet 28/32

382	268	2114	-4241	20	1894	-630	232	-2390	-3421	223	1430	762	-4307	17	-3539	-3281	1630	-2291	377	-815	535
-	-149	-500	233	43	-381	399	106	-628	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
383	-86	-3754	-986	-2134	-253	2389	-2380	-1076	-705	-3711	-2881	-246	-3791	-531	-2512	755	-2599	-3301	3597	561	
-	-149	-500	233	43	-381	399	106	-628	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1	-10485	-11527	-894	-1115	-701	-1378	-4124	785	-1746	725	167	902	-1802	-59	-911	-2560	-1720	353	-177	
384	237	-4070	1550	-54	-92	1244	-2259	-4124	785	-1746	-720	275	394	45	96	359	117	-369	-294	-249	
-	-149	-500	233	43	-381	399	106	-628	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-72	-10485	-4386	-894	-1115	-701	-1378	-1612	739	-1661	-3118	1729	-1558	34	-1142	84	229	-611	-4213	-3531	
385	-63	-4029	2080	-1002	334	-1340	-117	-1612	739	-1661	-720	275	394	45	96	359	117	-369	-294	-249	
-	-149	-500	233	43	-381	399	106	-628	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-2	-10415	-11457	-894	-1115	-1898	-451	-201	987	-4047	-3120	312	1382	1007	1503	529	-2497	-1484	-4214	-3532	
386	-773	-4031	-704	-52	-4352	698	-2190	201	987	-4047	-720	275	394	45	96	359	117	-369	-294	-249	
-	-149	-500	233	43	-381	399	106	-628	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-881	-10415	-1133	-894	-1115	-1898	-451	-3373	-107	-1031	-2393	849	1084	-1008	474	1233	-55	-2925	-3488	-2808	
387	741	-3304	1598	-1134	-3623	-614	-1467	-3373	-107	-1031	-720	275	394	45	96	359	117	-369	-294	-249	
-	-149	-500	233	43	-381	399	106	-628	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1176	-9537	-847	-894	-1115	-4520	-64	-1205	-3308	-962	-2368	673	-2559	1497	-1539	-1496	-1645	-2848	-3420	-2662	
388	-1675	-3241	2685	911	-3524	547	-1205	-3308	-962	-2368	-720	275	394	45	96	359	117	-369	-294	-249	
-	-149	-500	233	43	-381	399	106	-628	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-893	-8368	-1126	-894	-1115	-5157	-41	-2015	1436	-1999	-1100	-219	560	202	-320	-492	1175	-1600	-2188	-1539	
389	1055	-1975	-432	972	-2289	-1557	-243	-2015	1436	-1999	-715	279	393	51	90	384	119	-375	-289	-243	
-	-151	-505	234	40	-386	407	100	-632	205	-471	-715	279	393	51	90	384	119	-375	-289	-243	
-	-2651	-632	-2354	-3521	-132	-4314	-74	-3308	-3117	-3599	-2716	-2079	-2284	-2759	-3042	1540	-1074	-2263	-3808	-3620	
390	3077	-1244	-3035	-3163	-3572	-1512	-2789	-3308	-3117	-3599	-721	277	393	45	95	359	117	-370	-285	-250	
-	-147	-500	232	45	-381	398	105	-627	212	-466	-721	277	393	45	95	359	117	-370	-285	-250	
-	-2640	-257	-8518	-44	-5048	-2662	-248	-2487	1705	-2473	1101	-712	-2156	-277	373	-974	-1017	396	-2674	1075	
391	837	-2471	292	1046	-2759	-2064	-726	-2487	1705	-2473	-720	275	394	45	96	359	117	-369	-294	-249	
-	-149	-500	233	43	-381	399	106	-628	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-6	-8461	-9503	-894	-1115	-5129	-42	-2480	-3727	986	-2078	188	-4225	-3165	-3598	-3353	-3036	-2449	2248	3302	
392	-3113	-2830	1818	-4013	1528	-4239	-1573	-2480	-3727	986	-720	275	394	45	96	359	117	-369	-294	-249	
-	-149	-500	233	43	-381	399	106	-628	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-6	-8461	-9503	-894	-1115	-5129	-42	-2480	-3727	986	-720	275	394	45	96	359	117	-369	-294	-249	
393	1024	-2812	841	-685	-3146	-2343	-968	-2875	723	-2815	875	-882	-2432	1215	2615	-1268	-1317	-2443	-2871	-2324	
-	-149	-500	233	43	-381	399	106	-628	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-5	-8715	-9758	-894	-1115	-5040	-45	-840	869	-2303	-1500	-1174	-2521	995	809	-1382	-1321	1849	2205	-2088	
394	-1389	-2365	-1493	1183	-2538	-2440	-1087	840	869	-2303	-720	275	394	45	96	359	117	-369	-294	-249	
-	-149	-500	233	43	-381	399	106	-628	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-5	-8715	-9758	-894	-1115	-3388	-145	-628	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
395	-252	-2857	465	727	-3178	-2365	-1023	659	1621	-2872	-1847	-1002	844	1191	1114	-1272	-1330	-2478	2000	-2361	
-	-149	-500	233	43	-381	399	106	-628	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-4	-8936	-9978	-894	-1115	-533	-1694	-3812	1798	872	321	-1971	-3421	504	1116	821	-2288	-3385	-3888	-3297	
396	835	-3773	288	-1664	-570	-3328	-71	-3812	1798	872	-720	275	394	45	96	359	117	-369	-294	-249	
-	-149	-500	233	43	-381	399	106	-628	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-2	-10162	-11204	-894	-1115	-608	-1540	-628	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	

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397	823	-3170	-879	-864	-3221	-1232	-2575	1277	-838	530	-193	-665	-3925	-2353	-177	-750	-116	986	-3543	1959	576
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
398	-2	-10384	-11428	-894	-1115	-2206	-353	-7	2491	-1778	797	-2145	-29	-526	1325	-1394	-495	-3619	-4184	-3503	577
-	-2534	-3999	1738	-525	-4317	-3509	-2167	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-2	-10384	-11428	-894	-1115	-699	-1380	-1220	-3309	2278	2476	66	-4253	1410	-3454	-795	-758	-2284	-3287	-2908	578
399	-258	-2854	-4113	-3531	-2836	-1419	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-2	-10447	-11489	-894	-1115	-369	-2148	-415	-4122	585	-1920	-4034	-4466	-750	-3952	-3496	-2818	-566	-3175	-681	579
400	2748	75	-1809	-4507	-2873	1064	-3284	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1	-10485	-11527	-894	-1115	-701	-1378	-1143	-4070	417	924	1587	-4454	-862	-171	-6	-794	-314	1884	2318	580
401	1007	-2722	-5068	-4442	-260	-922	-3266	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1	-10485	-11527	-894	-1115	-701	-1378	886	-1305	-185	571	-1288	-4343	-3320	-3627	-142	257	1282	-3287	-2900	581
402	2091	-2828	-4410	-350	-2798	-765	-3108	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1	-10485	-11527	-894	-1115	-701	-1378	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
403	-316	-2736	-5254	-4620	2973	-4458	-3317	833	-4215	1354	-1929	-4102	-4507	-3835	-4014	-1749	-2851	505	890	1656	582
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
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404	-2877	-2707	-5197	-688	-2661	-4422	-3292	2104	-4164	1293	2607	-4050	-4472	1015	-3972	-762	653	-558	870	-503	583
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1	-10485	-11527	-894	-1115	-701	-1378	-67	-4181	2348	1741	-1301	-4477	-259	-3983	-3512	-2821	-1289	-3164	-2822	584
405	-102	-249	-5221	-4585	1419	-4427	1872	-67	-4181	2348	1741	-1301	-4477	-259	-3983	-3512	-2821	-1289	-3164	-2822	
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1	-10485	-11527	-894	-1115	-701	-1378	-1241	-4015	817	573	-3987	-4463	-3694	-1461	860	2532	-2226	-3266	-2918	585
406	1121	-2789	-4966	-4359	-2774	272	-3299	-1241	-4015	817	573	-3987	-4463	-3694	-1461	860	2532	-2226	-3266	-2918	
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1	-10485	-11527	-894	-1115	-701	-1378	-705	-4168	978	1453	-1329	-4472	-3794	1338	1072	-2817	-857	2168	578	586
407	-1162	504	-5204	-4569	278	-1169	2392	-705	-4168	978	1453	-1329	-4472	-3794	1338	1072	-2817	-857	2168	578	
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1	-10485	-11527	-894	-1115	-701	-1378	-1792	-929	-1839	-3180	-524	2750	-56	1482	-863	-287	-1727	-4274	-3592	587
408	-197	-4091	834	483	-4411	-3593	-2252	-1792	-929	-1839	-3180	-524	2750	-56	1482	-863	-287	-1727	-4274	-3592	
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1579	-10485	-590	-894	-1115	-701	-1378	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
409	108	-1682	-2115	-1557	277	1324	-1460	-1493	-1415	-235	-1061	540	-2792	356	-1750	116	-1418	-1344	-2264	2967	588
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
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410	-1283	-4239	-1531	-5491	-6783	3626	-5827	-6578	-6019	-6793	-5871	-4794	-5195	-5548	-437	-1285	-4041	-1415	-8851	-6754	589
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-1	-10485	-11527	-894	-1115	-701	-1378	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
411	-811	-2728	-5019	-4396	-875	-4395	-346	1500	-4034	-2578	475	986	-4447	-712	-1081	19	2168	1087	647	877	590
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
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412	-463	-3750	-5545	-5211	-4778	-1375	-4850	-4375	-1470	-1705	-3960	-4554	3885	-4708	-5002	-885	-483	-587	-5170	-4852	-597	
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-	-1	-10485	-11527	-894	-1115	-701	-1378	504	-467	159	-2214	-493	-1071	784	174	-46	-1380	1009	-3440	1877	592	
413	-406	2352	-733	-3127	323	-4097	-2866	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249		
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249		
-	-1	-10485	-11527	-894	-1115	-701	-1378	3264	-8982	-3594	268	-6819	-6917	-6860	-7081	-6511	232	2105	-6428	-5951	593	
414	-4702	-4203	-7370	-7027	262	-7166	-7004	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249		
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249		
-	-1	-10485	-11527	-894	-1115	-701	-1378	-8013	-7401	-5320	1998	-5995	-7240	-538	-6768	-6634	-6976	-6169	-2818	4339	594	
415	-7127	-6045	-7502	-7856	2309	-7388	-309	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249		
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-	-1	-10485	-11527	-894	-1115	-701	-1378	-4733	-3410	-4822	-4070	-46	-4701	1972	-3807	1462	-3584	-4336	1028	3906	595	
416	-1722	-4302	-3604	-3359	-4183	-1214	-3510	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249		
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-	-1	-10485	-11527	-894	-1115	-701	-1378	-6677	-5288	-6784	-5927	-4169	-38	-4749	-53	525	-4212	-5576	-6941	-6442	596	
417	-1566	-4606	633	-4189	-6820	3298	-4973	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249		
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418	-2645	-4116	2070	1526	-1241	-3611	1940	-826	210	-466	-720	275	394	45	96	359	117	-369	-294	-249		
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-	-1	-10485	-11527	-894	-1115	-701	-1378	-4056	-681	-1825	1023	-542	-3702	-1821	-265	-1370	-1030	-1215	-4231	-936	598	
419	-2625	-4031	-1060	3238	-618	-1292	-2271	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249		
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249		
-	-1	-10485	-11527	-894	-1115	-701	-1378	1638	-4078	-417	905	-844	-4456	2001	-3927	-491	-2813	-331	2033	1810	599	
420	-1034	-2720	-5079	-1279	1571	-1417	58	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249		
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249		
-	-1	-10485	-11527	-894	-1115	-701	-1378	-4291	-2183	-1667	-3405	-2448	-1378	-2104	-2699	49	404	-3889	-4504	1570	600	
421	-2807	-4280	618	-862	-4563	2854	664	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249		
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249		
-	-50	-10485	-4914	-894	-1115	-701	-1378	-1113	-3495	-4	3600	-1012	-4294	413	445	-1247	-830	-1236	2804	382	601	
422	-474	598	-1486	-1922	308	-114	-3056	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249		
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249		
-	-2	-10437	-11479	-894	-1115	-328	-2299	-155	-238	-2200	-225	301	111	-578	-2341	744	2247	-1726	-4272	-3591	602	
423	238	-4087	1128	-891	-4408	-367	177	-155	-238	-2200	-225	301	111	-578	-2341	744	2247	-1726	-4272	-3591	602	
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249		
-	-125	-10485	-3606	-894	-1115	-701	-1378	-51	-409	-3083	1846	-3587	-162	-2243	-2402	-424	-3615	-4177	638	603		
424	-1091	-3993	833	-617	75	2430	-131	-4063	-51	-409	-3083	1846	-3587	-162	-2243	-2402	-424	-3615	-4177	638	603	
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249		
-	-2	-10362	-11404	-894	-1115	-2391	-305	-4054	328	-4000	-3073	48	-566	613	2233	-560	-473	500	-4168	393	604	
425	-378	-3984	1222	-100	601	1631	-153	-4054	328	-4000	-3073	48	-566	613	2233	-560	-473	500	-4168	393	604	
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249		
-	-30	-10362	-5680	-894	-1115	-2391	-305	-166	-4033	1214	-3977	113	1373	475	-658	533	-106	-314	-3583	1877	258	605
426	127	-3961	870	-877	-4263	489	-166	-4033	1214	-3977	113	1373	475	-658	533	-106	-314	-3583	1877	258	605	
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249		
-	-1169	-10334	-851	-894	-1115	-2590	-282	-1169	-10334	-851	-894	-1115	-2590	-282	-1169	-10334	-851	-894	-1115	-2590	-282	

427	-459	-1653	-3572	-408	1776	1540	-2061	1132	-2865	-1506	970	-2687	-708	-294	-2842	-256	-1875	773	-2101	863	606
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-284	-249	
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-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-284	-249	
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439	-2407	3398	-136	1040	-4126	-1288	-2049	-3861	-1638	-267	-2922	-2032	-3481	-62	2733	-1148	-978	-3437	-4023	-448	633
-	-149	-500	233	43	-381	399	106	-628	210	-466	-720	275	394	45	96	359	117	-369	-284	-249	
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-	-188	-10255	-3060	-894	-1115	-1634	-438	-	-	-	-	-	-	-	-	-	-	-	-	-	

Table 4, Sheet 30/32

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Table 4, Sheet 31/32

[illegible]

Table 4, Sheet 32/32

**INDICATIONS RELATING TO DEPOSITED MICROORGANISM
OR OTHER BIOLOGICAL MATERIAL**

(PCT Rule 13bis)

A. The indications made below relate to the deposited microorganism or other biological material referred to in the description on page <u>54</u> , line <u>32</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution DSMZ - Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH	
Address of depositary institution (including postal code and country) DSMZ Mascheroder Weg 1b D-38124 Braunschweig Germany	
Date of deposit 15/09/2003	Accession Number DSM 15926
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit")	

<p align="center">For receiving Office use only</p> <p><input checked="" type="checkbox"/> This sheet was received with the international application</p> <hr/> <p>Authorized officer M. Samock: <i>MAN</i></p>	<p align="center">For International Bureau use only</p> <p><input type="checkbox"/> This sheet was received by the International Bureau on:</p> <hr/> <p>Authorized officer</p>
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INTERNATIONAL SEARCH REPORT

International Application No
PCT/EP2004/010985

A. CLASSIFICATION OF SUBJECT MATTER
IPC 7 C12N5/10 A01H5/00 C12N15/82 C12N9/10

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 7 C12N A01H

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, Sequence Search, BIOSIS, PAJ, WPI Data

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 01/70942 A (DANISCO ; POULSON PETER (DK); SOERENSEN IBEN SCHILDT (DK)) 27 September 2001 (2001-09-27) the whole document	1-17,22, 23,26-32
X	WO 96/34968 A (GIDLEY MICHAEL JOHN ; WESTCOTT ROGER JOHN (GB); COOKE DAVID (GB); DEBE) 7 November 1996 (1996-11-07)	1-17,22, 23,26-32
X	example 25 example 1 page 28 page 39, paragraph 3 claims 1-68	18,23-26
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☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

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- *O* document referring to an oral disclosure, use, exhibition or other means
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Date of the actual completion of the international search

11 January 2005

Date of mailing of the international search report

18/01/2005

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INTERNATIONAL SEARCH REPORT

International Application No
PCI/EP2004/010985

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>DATABASE EMBL 'Online! 8 June 2001 (2001-06-08), "EST512701 cSTD Solanum tuberosum cDNA clone cSTD203 5' sequence, mRNA sequence." XP002309391 retrieved from EBI accession no. EM_PRO:BG886850 Database accession no. BG886850 abstract</p>	18-20,23
A	<p>DATABASE UniProt 'Online! 1 March 2003 (2003-03-01), "Putative 1,4-alpha-glucan branching enzyme." XP002309392 retrieved from EBI accession no. UNIPROT:Q8GWK4 Database accession no. Q8GWK4 abstract & DATABASE EMBL SEQUENCE LIBRARY 13 December 2002 (2002-12-13), SEKI, M., ET AL.: "A. thaliana At3g20440 mRNA for putative 1,4-alpha-glucan branching enzyme, complete cds, clone: RAFL21-11-008" accession no. WWW.EBI.AC.UK Database accession no. AK118785 abstract</p>	
A	<p>JOBLING STEPHEN A ET AL: "A minor form of starch branching enzyme in potato (Solanum tuberosum L.) tubers has a major effect on starch structure: Cloning and characterisation of multiple forms of SBE A" PLANT JOURNAL, vol. 18, no. 2, April 1999 (1999-04), pages 163-171, XP002309385 ISSN: 0960-7412 figure 3 page 166, left-hand column, paragraph 1</p>	
A	<p>LARSSON CLAS-TOMAS ET AL: "Molecular cloning and characterization of starch-branching enzyme II from potato" PLANT MOLECULAR BIOLOGY, vol. 37, no. 3, June 1998 (1998-06), pages 505-511, XP002309386 ISSN: 0167-4412 the whole document figure 2</p>	
	-/-	

INTERNATIONAL SEARCH REPORT

International Application No
PCT/EP2004/010985

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	<p>KHOSHNOODI JAMSHID ET AL: "The multiple forms of starch-branching enzyme I in Solanum tuberosum" EUROPEAN JOURNAL OF BIOCHEMISTRY, vol. 242, no. 1, 1996, pages 148-155, XP002309387 ISSN: 0014-2956 the whole document figure 1</p>	
A	<p>MIZUNO K ET AL: "ALTERATION OF THE STRUCTURAL PROPERTIES OF STARCH COMPONENTS BY THE LACK OF AN ISOFORM OF STARCH BRANCHING ENZYME IN RICE SEEDS" JOURNAL OF BIOLOGICAL CHEMISTRY, AMERICAN SOCIETY OF BIOLOGICAL CHEMISTS, BALTIMORE, MD, US, vol. 268, no. 25, 5 September 1993 (1993-09-05), pages 19084-19091, XP002014043 ISSN: 0021-9258 the whole document</p>	
A	<p>BLAUTH SUSAN L ET AL: "Identification of Mutator insertional mutants of starch-branching enzyme 1 (sbel) in Zea mays L" PLANT MOLECULAR BIOLOGY, vol. 48, no. 3, February 2002 (2002-02), pages 287-297, XP002309388 ISSN: 0167-4412 page 295, right-hand column, last paragraph - page 296, left-hand column</p>	
A	<p>BLAUTH SUSAN L ET AL: "Identification of Mutator insertional mutants of starch-branching enzyme 2a in corn" PLANT PHYSIOLOGY (ROCKVILLE), vol. 125, no. 3, March 2001 (2001-03), pages 1396-1405, XP002309389 ISSN: 0032-0889 page 1401</p>	
A	<p>FLIPSE E ET AL: "INTRODUCTION OF SENSE AND ANTISENSE CDNA FOR BRANCHING ENZYME IN THE AMYLOSE-FREE POTATO MUTANT LEADS TO PHYSICO-CHEMICAL CHANGES IN THE STARCH" PLANTA, SPRINGER VERLAG, DE, vol. 198, 1996, pages 340-347, XP009019570 ISSN: 0032-0935 the whole document page 346, right-hand column, last paragraph</p>	

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INTERNATIONAL SEARCH REPORT

International Application No.
PCT/EP2004/010985

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	<p>RYDBERG ULRIKA ET AL: "Comparison of starch branching enzyme I and II from potato" EUROPEAN JOURNAL OF BIOCHEMISTRY, vol. 268, no. 23, December 2001 (2001-12), pages 6140-6145, XP002309390 ISSN: 0014-2956 the whole document</p> <p style="text-align: center;">-----</p>	

INTERNATIONAL SEARCH REPORT

International Application No
PCT/EP2004/010985

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 0170942	A	27-09-2001	GB 2360521 A 26-09-2001
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